

FIG. 1

jojobakcs 24 ATLPNFKSSINLHHVKL.GYHYLISNALFLVFIPLLGLASAHLSFSAHD 72
 .||| .| ::| :| :|:| . | | | | | ..
 ELO2 66 STLPPVLYAITAYVVIIFGGRFLLSKS..KPF.KLNGLFQLHNLVLTSL 112

jojobakcs 73 LSLFDLLRRNLLPVVVCSEFLFVLLATLHFLTRP 106
 |.|| |: |.::| |: : : |.|
 ELO2 113 LTLLL.LMVEQLVPIIVQHGLYFAICNIGAWTQP 145

FIG.2

S	T	L	P	P	P	V	L	Y	A	I	T	A	Y	Y	V	I	I	F	G	G	R	F	L
TCC	ACC	CTC	CCC	CCC	GTC	CTC	TAC	GCC	ATC	ACC	GCC	TAC	TAC	TAC	GTC	ATC	ATC	TTC	GGT	GGT	CGC	TTC	CTC
66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	

<--- RO339

L	S	K	S	K	P	F	K	L	N	G	L	F	Q	L	H	N	L	V	L	T	S	L
CTC	TCC	AAG	TCC	AAG	CCC	TTC	AAG	CTC	AAC	GGT	CTC	TTC	CAG	CTC	CAC	AAC	CTC	GTC	CTC	ACC	TCC	CTC
89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111

S	L	T	L	L	L	M	V	E	Q	L	V	P	I	I	V	Q	H	G	L	Y	F	
TCC	CTC	ACC	CTC	CTC	CTC	ATG	GTC	GAG	CAG	CTC	GTC	CCC	ATC	ATC	GTC	CAG	CAC	GGT	CTC	TAC	TTC	
112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134

A	I	C	N	I	G	A	W	T	Q	P
GCC	ATC	TGC	AAC	ATC	GGT	GCC	TGG	ACC	CAG	CCC
135	136	137	138	139	140	141	142	143	144	145

FIG.3

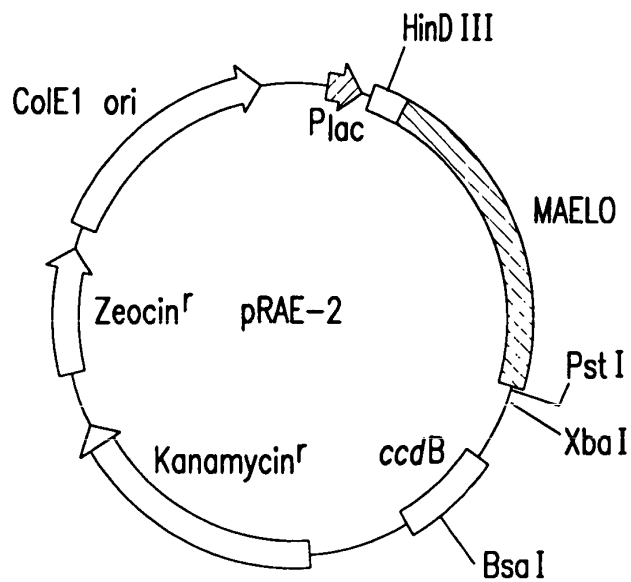


FIG.4A

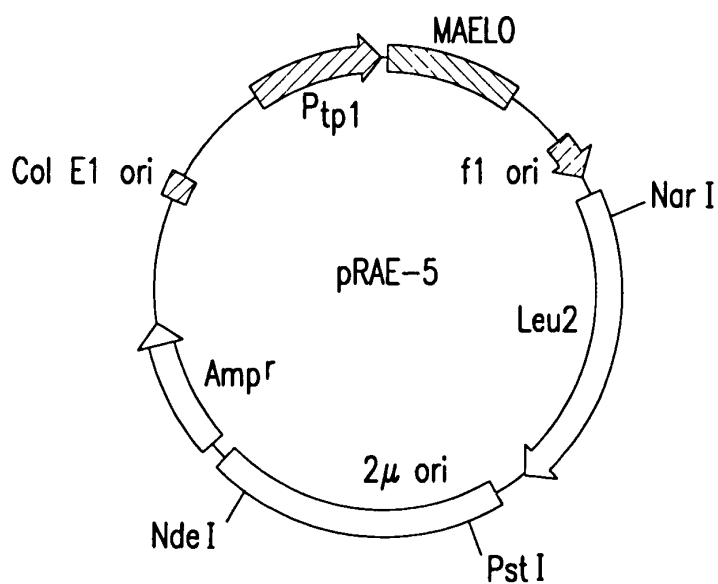


FIG.4B


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1  ATGGCCGCCG CAATCTTGGA CAAGGTCAAC TTCGGCATTG ATCAGCCCTT
51  CGGAATCAAG CTCGACACCT ACTTTGCTCA GGCTATGAA CTCGTACCG
101  GAAAGTCCAT CGACTCCTTC GTCTCCAGG AGGGCGTCAC GCCTCCTCG
151  ACCCAGAGAG AGGTCGCCAT GTGGACTATC ACTTACTTCG TCGTCATCTT
201  TGGTGGTCGC CAGATCATGA AGAGCCAGGA CGCCTTCAAG CTCAAGCCCC
251  TCTTCATCCT CCACAACTTC CTCCTGACGA TCGCGTCCGG ATCGCTGTTG
301  CTCCCTGTTCA TCGAGAACCTT GGTCCCATC CTCGCCAGAA ACGGACTTTT
351  CTACGCCATC TCGGACGACG GTGCCCTGGAC CCAGCGCTC GAGCTCCTCT
401  ACTACCTCAA CTACCTGGTC AAGTACTGGG AGTTGGCCGA CACCGTCTTT
451  TTGGTCCCTCA AGAAGAAGCC TCTTGAGTTC CTGCACACTT TCCACCACTC
501  GATGACCATG GTTCTCTGCT TTGTCCAGCT TGGAGGATAC ACTTCAGTGT
551  CCTGGGTCCC TATTACCCTC AACTTGACTG TCCACGTCTT CATGTACTAC
601  TACTACATGC GCTCCGCTGC CGGTGTTCCG ATCTGGTGGA AGCAGTACTT
651  GACCACTCTC CAGATCGTCC AGTTCGTTCT TGACCTCGGA TTCACTACTT
701  TCTGCGCCTA CACCTACTTC GCCTTCACCT ACTTCCCCTG GGCTCCCAAC
751  GTCGGCAAGT GCGCCGGTAC CGAGGTGCT GCTCTCTTTG GCTGCGGACT
801  CCTCTCCAGC TATCTCTTGC TCTTTATCAA CTTCTACCGC ATTACCTACA
851  ATGCCAAGGC CAAGGCAGCC AAGGAGCGTG GAAGCAACTT TACCCCCAAG
901  ACTGTCAAGT CCGGCGGATC GCCCAAGAAG CCTTCCAAGA GCAAGCACAT
951  CTAA

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FIG. 6

1 MAAAILDKVN FGIDQPFQIK LDYFAQAYE LVTGKSIDSF VFQEGVTPLS
51 TQREVAMWTI TYFVVIFGGR QIMKSQDAFK LKPLFILHNF LLTIASGSLL
101 LLFIENLVPI LARNGLFYAI CDDGAWTQRL ELLYYLNYLV KYWELADTVF
151 LVLKKKPLEF LHYFHHMTM VLCFVQLGGY TSVSWVPITL NLTVHVFMYY
201 YYMRSAAGVR IWWKQYLTTL QIVQFVLDLG FIYFCAYTYF AFTYFPWAPN
251 VGKCAGTEGA ALFGCGLLSS YLLLFINFYR ITYNAKAKAA KERGSNFTPK
301 TVKSGGSPKK PSKSKHI *

FIG.7

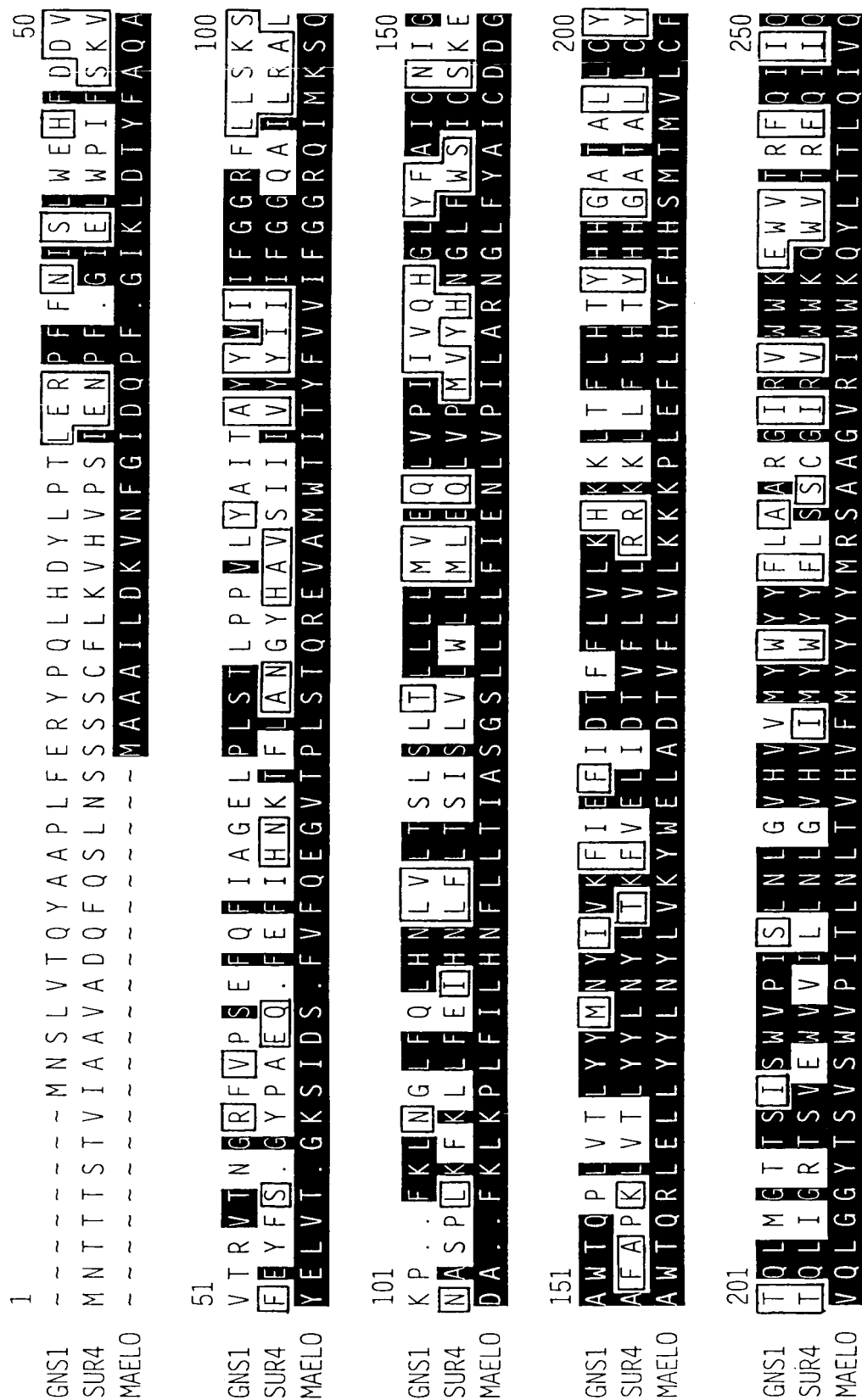


FIG.8A

251
 GNS1 FVLDLIGFIYFAVYQKAHLYFPILPHCGDCLVGSITTATFA GCAIISSYLV
 SUR4 FLIDLVFVYFAITFTFYAHKYLDGILPNKGTCTYGTQAAYAYGLITSYLL
 MAELO FVLDLGFIFYFCAYTYFAFTYFPWA.PNVGKCAGTEGALFGCGLLSSYLL

301
 GNS1 LFIIFYINVKRGTKTSRVVKRAHGGVAACKVNEYVNVDLKNVPTPSPSP
 SUR4 LFIIFYIQSKKGGKKTVKKESVSG.SVASSGSTGVKTNTKVS SRKA~
 MAELO LFIIFYRITYNAKAKAKERGSNFTPKTVKSGGSPK.KPSKSKHI*~ ~ ~

351
 GNS1 K P Q H R R K R
 SUR4 ~ ~ ~ ~ ~ ~ ~
 MAELO ~ ~ ~ ~ ~ ~ ~

FIG.8B

MAELO	150	160	170	180	190	200
	TCTCGACCCAGAGAGAGGTGCGCCATGTGGACTATCACTTACTTCGTGTCATCTTTGGTG					
S78624						
	CATTAAGCACTTTGCCCCCTGTGCTATACGCCATCACTGCCTATTACGTTATTTT					
	5990	6000	6010	6020	6030	6040
MAELO	210	220	230	240	250	260
	GTGCGCAGATCATGAAGAGCCAG--GACGCC-TTCAAGCTCAACCCCTCTTCATCCTCC					
S78624						
	GTGCGCAGGTTTGTAAAGTAAGTCGAAACCATTTAATTAATGGCCTTTTCCTCAATTGC					
	6050	6060	6070	6080	6090	6100
MAELO	270	280	290	300	310	320
	ACAACTTCCTCCTGACGATCGCGTCC--GGATCGCTGTGCTCCTGTTCATCGAGAACCT					
S78624						
	ATAAATTGGTTTAAAC-TTCACCTTTCATTGA-CGCTTTTATTGCTTATGGTTGAACAATT					
	6110	6120	6130	6140	6150	6160
MAELO	330	340	350	360	370	380
	GGTCCCCCATCCTCGCCAGAAACGGACTTTTCTACGCCATCTGCGACGACGGTGCCCTGGAC					
S78624						
	AGTGCCCAATTATTGTTTCAGCACGGGTTATACTTCGCTATCTGTAATATTGGTGCTTGGAC					
	6170	6180	6190	6200	6210	6220

FIG.9A

MAELO	390	400	410	420	430	440
	CCAGCGCCTCGAGCTCCTCTACTACCTCAACTACCTGGTCAAGTACTGGGAGTTGGCCGA					
S78624						
	TCAACCGCTCGTTACATTATATTACATGAATTACATTGTCAGTTTATTGAATTTATAGA					
	6230	6240	6250	6260	6270	6280
MAELO	450	460	470	480	490	500
	CACCGTCTTTTGGTCCCTCAAGAAGAGCCCTCTTGAGTTCCCTGCCTACTTCCACCACATC					
S78624						
	CACCTTTTCTTGGTGCTAAACATATAAAATTTGACATTTTGTGA-TACTT--ATCA--C					
	6290	6300	6310	6320	6330	6340
MAELO	510	520	530	540	550	
	GATGACCATGGTTCTCTGCTTTGT-----CCAGCTTGGAGGATA-CACTTCAGTGTCTCTGG					
S78624						
	CATGGCGCTACTGCCCTTATTATGTTACACCCCAATTGATGGGCACCACATCTATTCTTTGG					
	6350	6360	6370	6380	6390	6400
MAELO	560	570	580	590	600	610
	GTCCCTATTACCCCTCAACTTGACTGTCCACGTCTTTCATGTACTACTACTACATGCGCTCC					
S78624						
	GTCCCTATTTCATTGAACCTTGGTGTTCACGTGGTTATGTATTGGTACTATT---CTTG					
	6410	6420	6430	6440	6450	

FIG.9B

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	620	630	640	650	660	670
MAELO	GCTGCC	GGTGTCGCATCTGGTGAAGCAGTACTTGACCACTCTCCAGATCGTCCAG				
S78624	GCTGCCAGAGGCATCAGGGTCTGGTGAAGGAAATGGGTTACCCAGATTTCAAATTAATCCAA					
	6460	6470	6480	6490	6500	6510
	680	690	700	710	720	730
MAELO	TTCGTTCTTGACCTCGGATTCACTCTACTTCGCGCCTACACCTACTTCGCCCTTCACCTAC					
S78624	TTTGTTTTGGATATCGGTTTTCATATATTTTGCTGTCTACCAAAAAGCAGTTCACCTTGAT					
	6520	6530	6540	6550	6560	6570

FIG.9C

Host(plasmid)	334(pCGN7875)	334(pYES2)	334(pYX242)	334(pRAE-5)	334(pRAE-6)	334(pYX242)	334(pRAE-5)
Added substrate	25 μ M OA	25 μ M OA	25 μ M GLA	25 μ M GLA	25 μ M GLA	no substrate	no substrate
Fatty acid	lipid (μ g)	lipid (μ g)	lipid (μ g)	lipid (μ g)	lipid (μ g)	lipid (μ g)	lipid (μ g)
C16:0	11.948	23.601	35.123	92.011	85.160	16.294	25.34
C16:1	30.665	71.217	32.789	315.464	115.456	56.183	113.913
C18:0	6.185	9.704	10.515	22.628	18.879	5.535	11.092
C18:1n-9	35.340	57.429	33.989	154.386	106.881	28.388	51.538
C18:3n-6			48.856	58.084	12.434		
C20:0			0.474	0.710	0.244		
C20:1n-9	(0.375%)* 0.352	(0.309%)* 0.527		1.405	0.867		0.516
C20:3n-6	ND	ND	(0.092%)* 0.226	(0.324%)* 2.504	(0.269%)* 1.006	ND	ND
C22:0				0.460			
C22:1n-9				0.321	0.315		
C24:0					1.825		0.999
Total Lipid	93.760	170.490	245.090	771.690	374.420	112.99	256.52
ND = Not Detected							
*% total fatty acid							

FIG.10A

Host(plasmid)	334(pYX242)	334(pYX242)	334(pRAE-5)	334(pRAE-5)	334(pRAE-6)
Added substrate	25 μ M GLA	25 μ M GLA	25 μ M GLA	25 μ M GLA	25 μ M GLA
Fatty acid	lipid (μ g)	lipid (μ g)	lipid (μ g)	lipid (μ g)	lipid (μ g)
C16:0	60.683	61.487	100.998	96.193	66.761
C16:1	79.838	79.586	359.754	220.440	87.359
C18:0	9.784	10.106	15.317	15.165	16.744
C18:1n-9	38.536	39.936	108.472	89.637	71.631
C18:3n-6	17.974	17.833	82.866	56.596	17.766
C20:0			0.510	0.570	
C20:1n-9					
C20:3n-6	(0.136%)* 0.389	(0.130%)* 0.374	(0.336%)* 3.035	(0.401%)* 2.689	(0.353%)* 1.185
C22:0			0.414		
C22:1n-9				0.383	
C24:0			1.513	1.626	
Total Lipid	285.560	288.045	902.560	671.113	335.496
*% total fatty acid					

FIG.10B

Host(plasmid)	334(pRAE-5/pCGR4)	334(pYX242/pYES2)	Host(plasmid)	334(pRAE-5/pCGR4)	334(pYX242/pYES2)
Added substrate	25 μ M GLA	25 μ M GLA	Added substrate	25 μ M GLA	25 μ M GLA
Fatty Acid	lipid (μ g)	lipid (μ g)		lipid (μ g)	lipid (μ g)
C16:0	41.050	37.169	C16:0	96.986	32.221
C16:1	99.393	100.552	C16:1n-7	209.667	62.757
C18:0	34.432	27.852	C18:0	80.418	14.027
C18:1	110.631	92.786	C18:1n-9	207.104	28.701
C18:3n-6	15.004	7.924	C18:3n-6	25.264	10.543
C20:0	0.643	0.574	C20:0	2.038	
C20:1	1.996	1.684	C20:1n-9	3.591	
C20:3n-6	0.542	0.607	C20:3n-6	1.284	0.326
C20:4n-6	0.579		C20:4n-6	1.392	
C22:0	1.242	2.604	C22:0	1.124	
C24:0	4.754	4.563	C24:0	3.952	
Total Lipid	334	300	Total Lipid	756	197

FIG.11

Host(plasmid)	334(pYX242)	334(pRAE-5)	334(pRELO-1)	334(pRELO-2)
Added substrate	25 μ M GLA	25 μ M GLA	25 μ M GLA	25 μ M GLA
	25°C/48hrs	25°C/48hrs	25°C/48hrs	25°C/48hrs
Fatty acid	lipid (μ g)	lipid (μ g)	lipid (μ g)	lipid (μ g)
C16:0	28.7	76.707	84.424	77.445
C16:1	0.729	2.513	1.532	1.056
C18:0	7.432	15.761	27.17	21.32
C18:1n-9	28.9	77.323	109.419	82.844
C18:3n-6	9.729	29.236	19.085	18.804
C20:0		0.643	0.522	0.537
C20:1n-9		0.77	0.426	0.299
C20:3n-6	(0.185%)* 0.374	(0.279%)* 1.472	(0.153%)* 0.748	(0.200%)* 0.832
C22:0		0.451		
C22:1n-9			0.224	
C24:0		0.918		
Total Lipid	202	527	490	416
*%total fatty acid				

FIG.12

U61954	10	20	30	40	50	60	RTFKMMDQILGTNFTYEGAKEVARGLEGSAKLAVGYIATIFGLKYMKDRKAFDLSTPL
MAELO	30	40	50	60	70	80	AQAYELVTGKSIDSFVQEGVTPLSTQREVAMWTITYFVVI FGGRQIMKSQDAFKLK-PL
U61954	70	80	90	100	110	119	120
MAELO	90	100	110	120	130	FILHNFLLTIASGSLLLLFIENLVPI LARNGL-----FYAICDDGAWTQRLELLYY	
U61954	130	140	150	160	170	170	LWVISKIPELLDTVFIVLRKRPLIFMHWYHHALTGYALVCYHE--DAVHMVWV-VWMNY
MAELO	140	150	160	170	180	190	LNLYVKYWELADTVFLVLKKKPLEFLHYFHHSMT---MVLCFVQLGGYTSVSWVPITLNL

FIG. 13A

U61954	180	190	200	210	220	230
	IIHAFMYGYLLKSLKVP	IPPSVAQA	ITTSQMVQFA	-----VAIFAQVHVSYKH	YVEGVE	
	:	:	:	:	:	:
MAELO	TVHVFMYYYMRSAAGVRI	--WWKQYL	TTLQIVQFVLDL	GFIFYFCAYTYFA	TYFPWPAPN	
	200	210	220	230	240	250
U61954	240	250	260	270	280	
	-GLAYSFRGTAI	-GFFMLTTYFYLW	IQFYKEHYLKN	GKKYNLAKDQAK	TQTKKAN	
		:	:	:	:	:
MAELO	VGKCAGTEGAALFGCGL	LLSSYLLLF	INFYRITY	-----NAKAKA	KERGSNFTPK	TVKSGG
	260	270	280	290	300	
MAELO	SPKKPSKSKHIX					
	310					

FIG. 13B

Z68749	50	60	70	80	90	100
	SLLTNQDEVPHIRARRFIQEHFGLFVQMAIAYVILVFSIKRFMRDREPFQLTTALRLWN					
MAELO	ELVTGKSIDSFVFQEGVTPLSTQREVAMWTITYFVVFIFGGRQIMKSQDAFKLKPLFILHN					
	30	40	50	60	70	80
Z68749	110	120	130	140	150	160
	FFLSVFSIYGSWTMFPF--MVQQIRLYGLYGCCEALSNLPSQA EYWLFLTILSKAVEFV					
MAELO	FLLTIAS--GSLLLLFIEIENLVPILARNGLFYAICDD-GAWTQRLELLYYLNYLVKYWELA					
	90	100	110	120	130	140
Z68749	170	180	190	200	210	220
	DTFFLVLRKKPLIFLHWYHHMATFVFEC SNYPTPSSQSRVGVIVNL FVHAFMYPYFTRS					
MAELO	DTVFLVLRKKPLEFLHYFHHSM TMVLCFVQLGGYTSVSWVPITLNLTVHVFMYYYM RSA					
	150	160	170	180	190	200

FIG. 14A

Z68749	230	240	250	260	270
	MNIKVP	AKISMA	VTVLQ	LTQF---	MCFIYG
					CTLMYY
					SLATNQ
					ARYPSN
					TPATLQ
					CLSYTL
MAELO	210	220	230	240	250
	AGVRIW	WK--QY	LTTLQI	VFVLDL	GFIFYF
					CAAYTY
					FAFTYF
					FPWAPN
					VGKCA
					GTEGAA
					LFG
Z68749	280				
	HLL				
MAELO	270	280	290	300	310
	CGLLS	SYLL	LLFI	NFYRI	TYNA
					KA
					KA
					AKA
					K
					ERG
					SNFT
					PKTVK
					SGG
					SPKK
					PSK
					SKHIX

FIG. 14B

AF003134	10	20	30	40
	MYSITRRRCYTFVTSLSHFYQLYVTECLENVFNVLVNGQSINSRWKD			
	: : : : : : : : : : : :			
MAELO	10	20	30	40
	MAAAILDKVNFGIDQPPFGIKLDITYFAQA---YELVTGKSIDSFVFQEGVT---PLSTQREV			
	10	20	30	40
	50	60	70	80
	90	100	110	
AF003134	AEKTITSFPFHF-----PQTFQOPHILTLHFLFFVFSVTLVTVFKKPKCEFPHSLA			
	: : : : : : :			
MAELO	60	70	80	90
	AMWTITYFVVIFGGRQIMKSQDAFKLPLFILHNFLLTIASGSLLLFIENLVPILARNG			
	60	70	80	90
	100	110		

FIG.15

Mouse

U97107
MDTSMNFSRGLKMD--LMQPYDFETFDLRLPFLFEYVWVSF-----LIVV
|::| : | :: | :: | :: | :: | ::
MAAAILDKVNFGIDQPFGIKLDITYFAQAYELVTGKSIDSFVQEGVTFPLSTQREVAAMWTI
10 20 30 40 50 60

U97107
VYLLLVGQTYMRTRKSFSLQRPLILWSFFLAIFSI LGLTLMWKFMATVMFTVLGKQTIV
: : : : | :
TYFVVI FGGRQIMKSQDAFKLKLFLHNFLLITIAS--GSL-LILLFIENLV-PILARNGL

MAELO

```
U97107      110       120       130       140       150
CEAIYTD DAVRFWSEFLSKV----ELGDTAFIILKRPLIFVHWYHST--VLLFTS
          :|| | | ::   ::| :| ||::| ::| ::| ::| ::| ::| ::| ::|
MÆLO        FYAICDDGA WTORLELLYYINLVKYWE LADTVFVLKKKPLEFLHYFHHSMTWLCFVQ
          120     130    140    150    160    170
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FIG. 16A

Mouse

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160      170      180      190      200      210
U97107  FGYNKVPSSGWF-MTMNFGVHSVMTYYTMTKAAKLKHPNLLPMVITSLQILQMVLG----
        :|::| :|:|: || || || :|| :: :|:|:|:|:|:|
MAELO   LGGYTSV----SWVPITLNLTVHVMYYYYYMRSAAGVR--IWWKQYLTTLQIVQFVLDLGF
180      190      200      210      220      230

        220      230      240      250      260
U97107  -----TIFGIILNYIWRQEKG-CHTTTEHFHFWSEFMYGYTYFILFAHFFHAYLRPKGKVA
        | |:: :| :|:| | | ::| :|:|:|:|:|:| :|:|
MAELO   IYFCAYTYFAFTYFPWAPNVGKAGTEGAALFGCGLLSSYLLLETFNYRITY-NAKAKAA
        240      250      260      270      280      290

        270
U97107  SKSQX
        ::
MAELO   KERGSNFTPKTVKSGGSPKKPSPKSKHIX
        300      310

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FIG. 16B

Human	110	120	130	140	150	160
MAELO	NLVPILARNGLFYAICDDGAWTORLELLYYINYLKYYWEIADTVFLVLKKKPLEFLHYEH					
AC004050			SLLVVKDLTYLLPLCLPGDTIFIILRKQKLIFLHWHYH			
			10	20	30	
MAELO	170	180	190	200	210	220
	HSMTMVLCHFVLGGYTSVSWVPITINLTVHVFMYYYMRSAAAGVRIWKK--QYLTLQIV					
AC004050			HITVLLYSWYSYKDMVAGGGWFMTMNYGVHAVMYSYYALRAAGFRVSRKFAMFITLSQIT			
	40	50	60	70	80	90
MAELO	230	240	250	260	270	280
	QFVLDLGFIYFCAYTYFAFTYFPWAPNVGKCAGTEGAALFGCLLSSYLLLFINFYRITY					
AC004050			QMLMG-----CVVNYLVFC---WMQH-DQCHSHFQNIWFSSIMYLSYLVLFCHFFFEAY			
	100	110	120	130	140	

FIG. 16C

MAELO	40	50	60	70	80	90
	SFVFQEGV	PLSTQREV	AMWTITYF	VVIFGGRQ	IMKSQDAF	KLKPLFI
						LHNFLLT
						IASGS
I05465	20	30	40	50	60	70
	PRYKSQRM	VPPGQLHP	VVCLFCY	LLTHCMAG	TKIHEEPA	VLLPSILQ
						LYNLGLT
						LLS--
MAELO	100	110	120	130	140	150
	LLLLFIEN	LVPIIAR	NGLFYA	ICDDGAW	TQRLLE	LYL--
						NYLVKY
						WELADT
						VFLVLK
						KK
I05465	80	90	100	110	120	
	-LYMFYEL	VTGVWEG	KYNFFCQ	GTRSA	GESDMKI	IRVLW
						WVYF
						SKLIE
						FMDT
						FFFI
						LRKN
MAELO	160	170	180	190	200	210
	--PLEFL	HYFHH-S	MTMVL	CFVQL	GGYTSV	SWVPIT
						LNLT
						VHVFM
						YMYYY
						--MRS
						AAGVR
I05465	130	140	150	160	170	180
	NHQITV	LHVYH	HATML	NIWV	FVMNV	PCGHSY
						FGATL
						NSFI
						HVLM
						YSYGL
						SSIP
						SMRPY

FIG. 17A

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220      230      240      250      260      270
IWWKQYLTTLQIVQFVLDLGFYFCAYTYFAFTYFPWAPNVGKCAGTEGAALFGCGLLS
:||||:| |:||||| : :| : :| :| :| :| :| :| :| :| :| :| :| :| :|
LWWKKYITQGQLVQFVLT-IQTTCG-----VFWP-----CSFPLGWLFFQIGYMIS
190      200      210      220      230

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MAELO

I05465

```

280      290      300      310
YLLLFINFYRITYNAKAKAAKERGSNFTPKTVKSGSPKPKSKKHIX
: || || || || | : : ::
LLIALFTNFYIQTYNKKGASRRKEHLKGHQNGSVAAVNGHTNSFPLENSVKPRKQKDXQ
240      250      260      270      280      290

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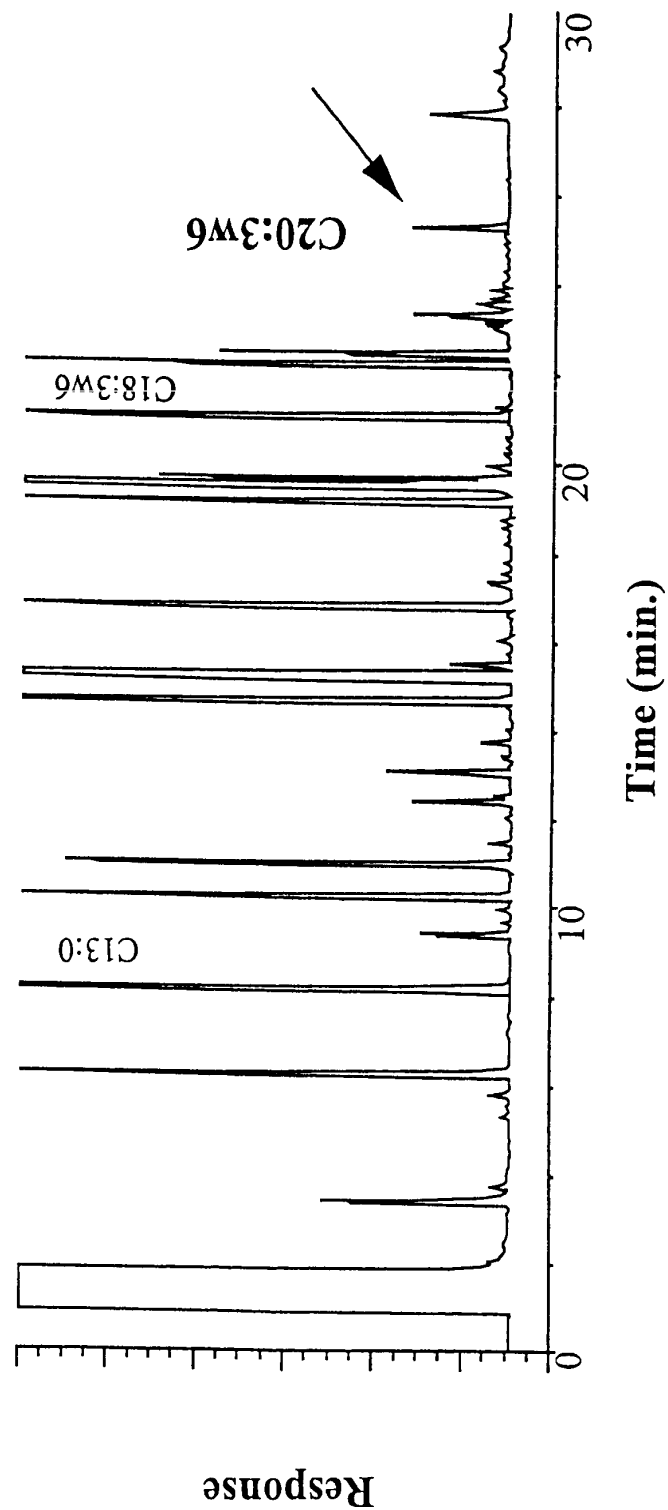
MAELO

I05465

FIG. 17B

1 MGTDQGKTFT WEELAAHNTK DDLALLAIRGR VYDVTKFLSR HPGGVDTLILL
51 GAGRDVTPVF EMYHAFGAAD AIMKKYYVGT LVSNELPIFP EPTVFHKTIK
101 TRVEGYFTDR NIDPKNRPEI WGRYALIFGS LIASYAQLF VPFFVERTWL
151 QVVFAIIMGF ACAQVGLNPL HDASHFSVTH NPTVWKILGA THDFFNGASY
201 LVWMYQHMLG HHPYTNIAGA DPDVSTSEPD VRRIKPNQKW FVNHNQHMF
251 VPFLYGLLAF KVRIQDINIL YFVKTNDAIR VNPISTWHTV MFWGGKAFFV
301 WYRLIVPLQY LPLGKVLLLF TVADMVSSYW LALTFQANH VEEVQWPLPD
351 ENGI IQDWA AMQVETTQDY AHDShLWTSI TGSLNYQAVH HLFPNVSQHH
401 YPDILAIKN TCSEYKVPYL VKDTFWQAFA SHLEHLRVLG LRPKEE*

FIG.18



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FIG.19

Host(plasmid)	334(MAD708-2)	334 (MAD708-10)	334(MAD708-18)	334 (MAD708-19)	334(MAD708-30)	334 (pRAE5)
Added substrate	25µM GLA	25µM GLA	25µM GLA	25µM GLA	25µM GLA	25µM GLA
Fatty Acid			% total lipid			
C16:0	14.1	14.68	14.38	15.45	14.13	13.59
C16:1	42.84	43.42	42.57	38.03	43.58	43.98
C18:0	3.19	3.28	3.63	4.08	3.37	2.04
C18:1n-9	17.66	19.39	19.6	20.8	20.06	10.88
C18:3n-6	6.65	5.58	10.24	9.46	3.56	11.14
C20:0	0.26	0.3	0.32	0.4	0.46	0.57
C20:3n-6	(47.5%) 6.03	(41.2%) 3.92	(8.0%) 0.91	(21.5%) 2.59	(49%) 3.43	(3.4%) 0.24
Total Lipid (µg)	238.47	307.86	188.51	167.31	207.47	466.65
(% conversion) = product/(substrate+product)						

FIG.20

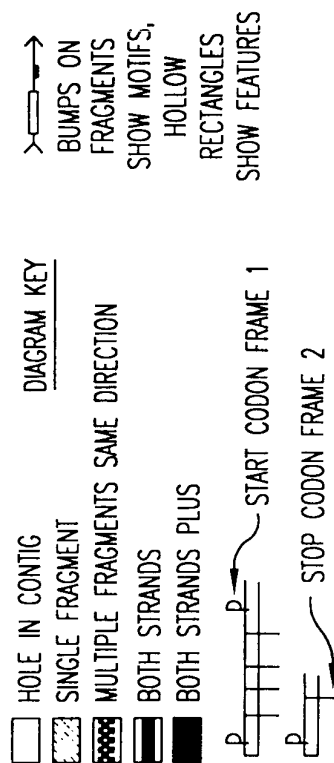


FIG. 21

```

1  ATGGAGTCTGA TTGCGCCATT CCTCCCATCA AAGATGCCGC AAGATCTGTT
51  TATGGACCTT GCCACCGCTA TCGGTGTCCG GGCCGCGCCC TATGTCGATC
101 CTCTCGAGGC CGCGCTGGTG GCCCAGGCCG AGAAGTACAT CCCACGATT
151 GTCCATCACA CGGTGGGTT CCTGGTCGG GTGAGTCCG CTTTGGCCCG
201 TGAGCTGCCG TTGATGAACC CGTTCCACGT GCTGTTGATC GTGCTCGCTT
251 ATTTGGTCCAC GGTCTTTGTG GGCATGCAGA TCATGAAGAA CTTTGAGCGG
301 TTCGAGGTCA AGACGTTTTC GCTCCTGCAC AACTTTGTG TGGTCTCGAT
351 CAGCGCCTAC ATGTGCGGTG GGATCCTGTA CGAGGCTTAT CAGGCCAACT
401 ATGGACTGTT TGAGAACGCT GCTGATCATA CCTTCAAGG TCTTCCATG
451 GCCAAGATGA TCTGGCTCTT CTACTTCTCC AAGATCATGG AGTTTGTCTGA
501 CACCATGATC ATGGTCCCTCA AGAAGAACAA CCGCCAGATC TCCTTCTTGC
551 ACGTTTACCA CCACAGCTCC ATCTTCACCA TCTGGTGGTT GGTACCTTT
601 GTTGCACCCA ACGGTGAAGC CTACTTCTCT GCTGCGTTGA ACTCGTTCAT
651 CCATGTGATC ATGTACGGCT ACTACTTCTT GTCGGCCCTG GGCTTCAAGC
701 AGGTGTCGTT CATCAAGTTC TACATCACGC GCTCGCAGAT GACACAGTTC
751 TGCATGATGT CGGTCCAGTC TTCCCTGGGAC ATGTACGCCA TGAAGGTCCT
801 TGGCCGCCCC GGATACCCCT TCTTCATCAC GGCTCTGCTT TGGTCTACA
851 TGTGGACCAT GCTCGGTCTC TTCTACAACT TTTACAGAAA GAACGCCAAG
901 TTGGCCAAGC AGGCCAAGC CGACGCTGCC AAGGAGAAGG CAAGGAAGTT
951 GCAGTAA

```

FIG. 22

1 MESIAPFLPS KMPQDLFMDL ATAIGVRAAP YVDPLEAALV AQAEKYIPTI
51 VHHTRGFLVA VESPLARELP LMNPFHVLLI VLAYLVTVFV GMQIMKNFER
101 FEVKTFSLLH NFCLVSISAY MCGGILYEAY QANYGLFENA ADHTFKGLPM
151 AKMIWLFYFS KIMEFVDTMI MVLKKNNRQI SFLHVYHHSS IFTIWWLVTF
201 VAPNGEAYFS AALNSFIHVI MYGYFFLSAL GFKQVSFIKF YITRSQMTQF
251 CMMSVQSSWD MYAMKVLGRP GYPFFITALL WFYMTTMLGL FYNFYRKNNAK
301 LAKQAKADAA KEKARKLQ*

FIG.23

Host(plasmid)	334(pRPB2)	334 (pYES2)
Added substrate	25μM GLA	25μM GLA
	(n=4)	
Fatty Acid	% total lipid	
C16:0	15.65	15.23
C16:1	35.2	38.59
C18:0	5.68	5.55
C18:1n-9	25.55	25.27
C18:3n-6	3.1	6.75
C20:0	0.36	0.14
C20:3n-6	(62.0%) 5.06	(2.6%) 0.18
Total Lipid (μg)	314	247
(% conversion) = product/(substrate+product)		

FIG.24

Host(plasmid)	334(pRPB2)	334(pRPB2)	334(pRPB2)	334(pRPB2)	334(pRPB2)	334(pRPB2)
Added substrate	25μM SA	25μM OA	25μM LA	25μM DGLA	25μM AA	25μM Adrenic
	C18:0	C18:1n-9	C18:2n-6	C20:3n-6	C20:4n-6	C22:4n-6
Fatty Acid	% total lipid					
C16:0	15.07	14.52	15.74	15.69	16.06	15.15
C16:1	33.7	32.37	32.23	25.65	33.65	33.39
C18:0	*9.78	5.83	5.61	8.33	4.52	5.35
C18:1n-9	31.2	*37.25	26.05	20.15	24.54	28.54
C18:2n-6			*10.4			
C18:3n-6						
C20:2n-6			0.29			
C20:3n-6				*16.5		
C20:4n-6				0.27	*11.7	
C22:4n-6						*7.46
Total Lipid (μg)	132	130	171	55	225	163

*indicates substrate added

(% conversion) = product/(substrate+product)

FIG.25A

Host(plasmid)	334(pRPB2)	334(pRPB2)	334(pRPB2)
Added substrate	25μM ALA	25μM STA	25μM EPA
	C18:3n-3	C18:4n-3	C20:5n-3
Fatty Acid	% total lipid		
C16:0	17.32	16.01	20.67
C16:1	27.68	34.31	50.7
C18:0	6.75	5.39	6.14
C18:1n-9	28.4	28.54	
C18:3n-3	*8.39		
C18:4n-3		*1.95	
C20:4n-3		(73.2%) 5.33	
C20:5n-3			*10.33
C22:5n-3			0.25
Total Lipid (μg)	114	199	201

*indicates substrate added
 (% conversion) = product/(substrate+product)

FIG.25B

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Host(plasmid)	334(pRPB2+PRPE31)	334(pYES2+pYX242)
Added substrate	25μM GLA	25μM GLA
Fatty Acid	% total lipid	
C16:0	15.54	18.26
C16:1	30.16	33.51
C18:0	8.76	5.58
C18:1n-9	27	27.37
C18:3n-6	*2.6	*5.6
C20:0	0.4	0.32
C20:3n-6	(57.4%) 3.55	(2.9%) 0.17
C20:4n-6	(27.6%) 1.32	ND
Total Lipid (μg)	254	258

* indicates substrate added

(% conversion) = product/(substrate+product)

FIG. 26A

Host(plasmid)	334(pRPB2+PRPE31)	334(pYES2+pYX242)
Added substrate	25μM STA	25μM STA
Fatty Acid	% total lipid	
C16:0	18	16.4
C16:1	28.37	34.78
C18:0	7.42	5.71
C18:1n-9	26.44	30.15
C18:4n-3	*2.93	*4.57
C20:0	0.25	0.17
C20:4n-3	4.13	0.32
C20:5n-3	(39%) 1.87	(2.1%) .10
Total Lipid (μg)	257	304

* indicates substrate added

(% conversion) = product/(substrate+product)

FIG. 26B

GLELO	40	50	60	70	80	90	99
	VAQAEKYIPTIVHHTRGFLVAVESPLAREPLMNPFFHVLIVLAYLVTVFVGMQIMKNFE						
MAELO				: : : : : : : : : : : : : :			
	GIKLDTYFAQAYELVTGKSIDSFVFQEGVTPPLSTQREVAMWTITYFVVFVIFGGRQIMKSQD						
	20	30	40	50	60	70	
GLELO	100	110	120	130	140	150	
	RFEVKTFSLHNFCLVSIAYMCGGILYE--AYQANYGLFENAADHTFKGLPMAKMIWLF						
MAELO		: : : : : : : : : : : : : :					
	AFKLKPLFILHNFLITIASGSLLLFIENLVPILARNGLFYAICDDGAWTQRLELLYYLN						
	80	90	100	110	120	130	
GLELO	160	170	180	190	200	210	
	YFSKIMEFVDVTMIMVLKKNRQISFLHVYHHSSIFTIWWLVTVFVAPNGEAYFSAALNSFI						
MAELO	: : : : : : : : : : : : : : :						
	YLVKYWELADTVFLVLKK--KPLEFLHYFHS-MTMVLCFVQLGGYTSVSWVPITLNLTV						
	140	150	160	170	180	190	

FIG. 27A

```

220      230      240      250      260
HVIMGYFLSALGFKQVSFIKFYITRSQMTQF-----CMMSVQS----SWDMYAM
||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
HVFMYYYMRSAAGVRI--WWKQYLTTLQIVQFVLDLGLFYFCAYTYFAFTYFPWAPNVG

```

GLELO

MAELO

270 280 290 300 310
 KVLGRPGYPFFITALLWFYMWMTMLGLFYNFYRKNAKLAKQAKADAKEKARKLQ
 | | | : | | : | | | | | : : | | | | | : :
 KCAGTEGAALFGCGLLSSYLL----LFINFYR----ITYNAKAKAAKERGSNFTPKTVKS
 260 270 280 290 300

GILLO

MAELO

GGSPKKPSKHX
310

MAELO

FIG. 27B

GLEO	1	-	M	E	S	I	A	P	F	L	P	S	K	M	P	Q	D	L	F	M	D	L	A	T	A	I	G	V	R	A	A	P	Y	V	D	P	L	E	A	A	L	V	A	Q	42
MAEO	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	20	
GNS1	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	36		
SUR4	1	M	N	T	T	T	S	T	V	I	A	A	V	A	D	Q	F	Q	S	L	N	S	S	S	S	C	F	L	K	V	H	V	P	S	I	E	N	P	-	F	G	I	E	L	42
GLEO	43	A	E	K	Y	I	P	T	I	V	H	H	T	R	G	F	L	V	A	V	E	S	P	L	A	R	E	L	P	L	M	N	P	F	H	V	L	L	I	V	L	A	Y	L	85
MAEO	21	L	D	T	Y	F	A	Q	A	Y	E	L	V	T	G	K	S	I	D	S	F	V	F	Q	E	G	V	T	P	L	S	T	Q	R	E	V	A	M	W	T	I	T	Y	F	63
GNS1	37	E	H	F	D	D	V	V	T	R	V	T	N	G	R	F	V	P	S	E	F	Q	F	I	A	G	E	L	P	L	S	T	L	P	P	V	L	Y	A	I	T	A	Y	Y	79
SUR4	43	W	P	I	F	S	K	V	F	E	Y	F	S	G	-	Y	P	A	E	Q	F	F	I	H	N	K	T	F	L	A	N	G	Y	H	A	V	S	I	I	I	V	Y	Y	84	
GLEO	86	V	T	V	F	V	G	M	O	I	M	K	N	F	E	R	F	E	V	K	T	F	S	L	L	H	N	F	C	L	V	S	I	S	A	Y	M	C	G	G	I	L	Y	E	128
MAEO	64	V	V	I	F	G	G	R	Q	I	M	K	S	Q	D	A	-	-	F	K	L	K	P	L	F	I	L	H	N	F	L	T	I	A	S	G	S	L	L	L	L	F	I	104	
GNS1	80	V	I	I	F	G	G	R	F	L	S	-	-	K	S	K	P	F	K	L	N	G	L	F	Q	L	H	N	L	V	L	T	S	L	S	L	T	L	L	L	M	V	120		
SUR4	85	I	I	I	F	G	G	Q	A	I	L	R	A	L	N	A	S	P	L	K	F	K	L	L	F	E	I	H	N	L	F	L	T	S	I	S	L	V	L	W	L	L	M	L	127
GLEO	129	-	-	A	Y	O	-	-	A	N	Y	G	L	F	E	N	A	A	D	H	T	F	K	G	L	P	M	A	K	M	I	W	L	F	Y	F	S	K	I	M	E	F	V	D	167
MAEO	105	E	N	L	V	P	I	L	A	R	N	G	L	F	Y	A	I	C	D	D	G	A	W	T	O	R	L	E	L	Y	Y	L	N	Y	L	V	K	Y	W	E	L	A	D	147	
GNS1	121	E	Q	L	V	P	I	I	V	Q	H	G	L	Y	F	A	I	C	N	I	G	A	W	T	Q	P	L	V	T	L	Y	Y	M	N	Y	I	V	K	F	I	E	F	I	D	163
SUR4	128	E	Q	L	V	P	M	V	Y	H	N	G	L	F	W	S	I	C	S	K	E	A	F	A	P	K	L	V	T	L	Y	Y	L	N	Y	L	T	K	F	V	E	L	I	D	170
GLEO	168	T	M	I	M	V	L	K	K	N	N	R	Q	I	S	F	L	H	V	Y	H	H	S	S	I	F	T	I	W	W	L	V	T	F	V	A	P	N	G	E	A	Y	F	S	210
MAEO	148	T	V	F	L	V	L	K	K	-	-	K	P	L	E	F	L	H	Y	F	H	H	S	M	T	M	V	L	C	F	-	V	O	L	G	Y	T	S	V	S	W	V	P	187	
GNS1	164	T	F	F	L	V	L	K	H	-	-	K	K	L	T	F	L	H	T	Y	H	H	G	A	T	A	L	L	C	Y	-	T	O	L	M	G	T	T	S	I	S	W	V	P	203
SUR4	171	T	V	F	L	V	L	R	R	-	-	K	K	L	L	F	L	H	T	Y	H	H	G	A	T	A	L	L	C	Y	-	T	Q	L	I	G	R	T	S	V	E	W	V	V	210

FIG.28A

GLEO	211	A A L N S F I H V I M Y G Y Y F L S A L G F K Q V S F I K F Y I T R S Q M T O F C M M	253
MAELO	188	I T L N L T T V H V F M Y Y Y M R S A A G V R - - I W W K Q Y L T T L O I V O F V L D	228
GNS1	204	I S L N L G V H V V M Y W Y Y F L A A R G I R - - V W W K E W V T R F O I I O F V L D	244
SUR4	211	I L L N L G V H V I M Y W Y Y F L S S C G I R - - V W W K Q W V T R F Q I I Q F L I D	251
GLEO	254	S V O S S W D M Y A M K V L G R P G Y P F F I T A L L W F Y M W T M L G L F Y N F Y R	296
MAELO	229	L G F I Y F C A Y T Y F A F T Y F P W - A P N V G K C A G T E G A A L F G C G L L S S	270
GNS1	245	I G F I Y F A V Y O K A V H L L Y F P - I L P H C G D C V G S T T A T F A G C A I I S S	286
SUR4	252	L V F V Y F A T Y T F Y A H K Y L D G I L P N K G T C Y G T Q A A A Y G Y L I L T S	294
GLEO	297	K N A K L A K O A K A D A A K E K A R K L Q	318
MAELO	271	Y L L L F I N F Y R I T Y N A K A K A K E R G S N F T P K T V K S G G S P K K P S K	313
GNS1	287	Y L V L F I S F Y I N V Y K R K G T K T S R V V K R A H G G V A A K V N E Y V N V D L	329
SUR4	295	Y L L L F I S F Y I Q S Y K K G G K K T V K K E S E V S G S V A S G S S T G V K T S N	337
MAELO	314	S K H I	
GNS1	330	K N V P T P S P S P K P Q H R R K R	
SUR4	338	T K V S S R K A	

FIG.28B


```

210      220      230      240      250      260
MRSAAGVR--IWKQYLTLQIVQFVLDLGFIYFCAYTYFAFTYFPWAPNVGKCAGTEGA
: |: :| :|||:| |: :||| : : |: | | |: |
LSSVPSMRPYLWKKYITQGQLLQFVLTI-IQTSCGVI-----W-P-----CTFPLGW
190      200      210      220      230

```

MAELO

TSH

	270	280	290	300	310
ALFGCGLLSSYLLFINFYRITYNAKAKAAKERGSNFTPKTVKSGGSPKPKSKHI					
: : : : :					
LYFQIGYMISLIAFLTNFYIQTYNKKGASRRKDLHKDHQNGSMAAVNGHTNSFSPLENNV	240	250	260	270	280 290

MAELO

TSH

HS1 KPRKLRKDX 300

FIG. 29B

MAELO	30	40	50	60	70	80
HS2	QAYELVTGKSIDSFVFQEGVTPLSTQREVAMWTITTYFVVFEGGRQIMKSQDAFKLKPLFLI	:	:	:	:	:
	10	20	30	40	50	60
MAELO	90	100	110	120	130	140
HS2	LHNFLTITIASGSLLLFIEN--LVPILAR-NGLFYAICDDGAWTQRLLELLYYLNYLVKYW	:	:	:	:	:
	70	80	90	100	110	120
MAELO	150	160	170	180	190	
HS2	ELADTVFLVLKKK--PLEFLHYFHHSMT---MVLCFVQLGGYTSVSWVPITLNLTVHVF	:	:	:	:	
	130	140	150	160	170	
MAELO	150	160	170	180	190	
HS2	ELMDTVIFILRKDGQVTFLLHVFHHSVLPWSWWMGVKIAPGGMGSFHAM---INSSVHVIT	:	:	:	:	

FIG. 30A

MAELO	200	210	220	230	240
	MYYYMRSAGV----	RIWKKQYLTTLQIVQFVL---	DLGFIYF---	CAYTYFAFTYFPW	
HS2	180	190	200	210	220
	MYLYYGLSAFGPVAQPYLWKKHMTAIQLIQFVLVSLHISQYYFMSSCNCYQYFVIIHLIW				
MAELO	250	260	270	280	290
	APNVGKCAGTEGAALFGCGLLSSYLLLFINFYRITYNAKAKAAKERGSNFTPKTVKSGGS				
HS2	240	250	260	270	280
	-----MYG-----	TIFFMLFSNFWYHSYTKGKRLLPRALQQQNGAPGIKVKAN			
MAELO	310				
	PKKPSKSKHI				
HS2					
	X				
	280				

FIG. 30B

MAELO	100	110	120	130	140	150	
	L L L L F I E N L V P I L A R N G L F Y A I C D D G A W T Q R L E L L Y L N L V K Y W E L A D T V F L V L K K P -						
MM2							
	I V Y E F L M S G W L S T Y T W R C D P I D F S N S P E A L R M V R V A W L F M L S K V I E L M D T V I F I L R K K D G						
	20	30	40	50	60	70	
MAELO	160	170	180	190	200	209	
	- L E F L H Y F H H S M I M V L C F - - - - V Q L G G Y T S V S W P I T I L N L T V H V F M Y Y Y M R S A A G V - - -						
MM2							
	Q V T F L H V F H H S V L P W S W W G I K I A P G G M G S F H A M - - - I N S S V H V M Y L Y Y G L S A L G P V A Q						
	80	90	100	110	120	130	
MAELO	210	220	230	240	250	260	
	- R I W W K Q Y L T T L Q I V Q F V L - - - D L G F T Y F - - - C A Y T Y F A F T Y F P W A P N V G K C A G T E G A A L						
MM2							
	P Y L W W K K H M T A I Q L I Q F V L V S L H I S Q Y Y F M P S C N Y Q Y P V I I H L I W - - - - - M						
	140	150	160	170			
MAELO	270	280	290	300	310		
	F G C G L L S S Y L L L F I N F Y R I T Y N A K A K A K E R G S N F T P K T V K S G S P K P S K S K H I						
MM2							
	Y G - - - - T I F F I L F S N F W Y H S Y T K G K R L P R A V Q Q N G A P A I T K V K A N						
	180	190	200	210			

FIG.31

MAELO	30	40	50	60	70	80
AI225632	YELVTGKSIDSFVFQEGVTPLSTQREVAMWTTITVVFVIFGGRQIMKSQDAFKLKPLFILH					
	NAFLDNMFGPRDSRVRGWFLLDSYLPYFILTITITVLLSIWLGKYMKNRPALSLRGILTLY	20	30	40	50	60
						70
MAELO	90	100	110	120	130	140
AI225632	NFLLTIAAGSLILLFIENLVPILARNGLFYAICDD----GAWTQRLLELLYYLNYLVKYWE					
	NLAITLLSAYMLVELI-----LSSWEGGYNLQCQNLDGAGEGDVVRVAKVLLVWYFVSKLVE	80	90	100	110	120
MAELO	150	160	170	180	190	200
AI225632	LADTFVLVLKKK--PLEFLHYFHHSMIMVLCFVQLGGYTSVSWVPITLNLTVHVFMYYYY					
	FLDTIFFVLKKKANQITFLHVYHHASMFNI	130	140	150		

FIG.32

GLELO	80	90	100	110	120	130	
AI815960	LIVLAYLVTVFVGMQIMKNFERFEVKTFSLHNFCLVSIAYMCGGILYEAYQANYGL-F						
	: : : : : : : : : : :						
	LYNLGITLLSAYMLAELILSTWEGGYNLQC						
		10	20	30			
GLELO	140	150	160	170	180	190	
AI815960	ENAAHTEFKGLPMAKMIWLFFYFSKIMEFVDTMIMVLKKNRQISFLHVYHHSSIFTIWWL						
	: : : : : : : : : : : : : : : : : : : : : : : :						
	QDLTSAGEADIRVAKVLWWYYFYSKSVFFLDTIFFVLRKRTSQITFLHVYHHASMFNIWWC						
	40	50	60	70	80	90	
GLELO	200	210	220	230	240	250	
AI815960	VTFVAPNGEAYFSAALNSFIHVIMYGYFLSAL-GFKQVSFIKFYITRSQMTQFCMMSVQ						
	: : : : : : : : : : : : : : : : : : : : :						
	VLNWIPCGQSFFGPTLNSFIHILMYSYGYGLSVFPPSMHKYLVWKKYLTQAQLVQF						
	100	110	120	130	140		
GLELO	260	270	280	290	300	310	
	SSWDMYAMKVLGRPGYPFFITALLWFYMWMTMLGLEFNYRKNNAKLAKQAKADAAKEKARK						

FIG.33

GLELO	50	60	70	80	90	100
	AQAEKYIPTIVHHTRGFLVAVESPLARELPLMNPFFHLLIVLAYLVTVFVGMQIMKNFER					
HS1	<div style="display: flex; justify-content: space-around;"> MEHFDASLSTYFKALLGPRDTRVKGWFLLDNYIPTFICSVIYLLIVLWLGPKYMRNKQP : : : : : : : : : : : : : : : : : : : : : : : : : </div>					
	10	20	30	40	50	
GLELO	110	120	130	140	150	159
	FEVKTFSLHNECLVSI SAYMCGILYEAYQANYGLF-ENAAADHTFKGLPMAKMIWLFYF					
HS1	<div style="display: flex; justify-content: space-around;"> FSCRGILVVYNLGLTLLSLYMFCELVGTGVWEGKYNFFCQGTRTAGESDMKIIRVLWWYF : : : : : : : : : : : : : : : : : : : : : : : : : </div>					
	60	70	80	90	100	110
GLELO	160	170	180	190	200	210
	SKIMEFVDTMIMVLKKNRQISFLHVYHHSSIFTIWWLVTFAVPNGEAYFSAALNSFIHV					
HS1	<div style="display: flex; justify-content: space-around;"> SKLIEFMDTFFFILRKNNHQITVLHVYHHASMLNIWWFVMNVPCGHSYFGATLNSFIHV : : : : : : : : : : : : : : : : : : : : : : : : : </div>					
	120	130	140	150	160	170
GLELO	220	230	240	250	260	270
	IMYGYFLSAL-GEKQVSFIKFYITRSQMTQFCMMSVQSSWDMYAMKVLGRPGYPFFITA					
HS1	<div style="display: flex; justify-content: space-around;"> LMYSYGLSSVPSMRPYLWWKKYITQGQLLQFVLTIQTS-----CGVIWPCTFPPLGWLY : : : : : : : : : : : : : : : </div>					
	180	190	200	210	220	230
GLELO	280	290	300	310		
	LLWFYMWITMLGLFYNFYRK--NAKLAKQAKADAKEKARKLQ					
HS1	<div style="display: flex; justify-content: space-around;"> FQIGYMISLIALFTNFYIQTYNKKGASRRKDLKDHQNGSMAAVNGHTNSFSPLENNVKP : : : : : : : : : : : : : : : : </div>					
	240	250	260	270	280	290

FIG.34

GLELO	140	150	160	170	180	190
AC004050	FENAAADHTFKGLPMAKMIWLFYFYSKIMEFVDTMIMVLKKNRQISFLHVYHHSSIFTIWW					
	::: : ::: :::					
	DTIFIILRK--QKLI FLHWYHHITVLLYSW					
				10	20	
GLELO	200	210	220	230	240	250
AC004050	LVTFVAPNGEAYFSAALNSFIHVIMYGYFFLSALGFKQVSFIKFYITRSQMTQFCMMSVQ					
	::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::					
	YSYKDMVAGGWF-MTMNYGVHAVMYSYALRAAGFRVSRKFAMFITSQITQMLMGCVV					
	30	40	50	60	70	80
GLELO	260	270	280	290	300	310
AC004050	SSWDMYAMKVLGRPGYPFFITALLW--FYMTTMLGLFYNFYRKN--AKLAKQAKADAAKE					
	: : :					
	NYLVFCWMQ--HDQCHSHF-QNIFWSSLMYLSYLVLFCHFFFEAYIGKMRKTTKAEX					
	90	100	110	120	130	140

GLELO KARKLQ

FIG.35

GLELO	80	90	100	110	120	130
	LLIVLAYLVTVFVGMQIMKNFERFEVKTFSLHNFCLVSI	SAYMCGGILYEAYQANYGLF				
MM2				::: : :	: : : : :	
				IVYNFSLVILSLYIVYEFIMSGWLSTYTW		
				10	20	30

```

GLELO      140      150      160      170      180      190
ENAAD--HTFKGLPMAKMIWLFYFSKIMEFVDTMIMVLKKNNRQISFLHVYHHSSIFTIW
      : | :: :: |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
MM2        CDPIDFSPEALRMVRVAWLFMLSKVIELMDTVIFILRKDGQVTFLHVFHHSVLPWSW

```

[illegible]

	260	270	280	290	300	309
GLELO	SVQSSWDMYAMKVLGRPGYPFFITALLWFYMWTTMLGLFYNF----	YRKNAKLAKQAKADA				
	:: :: :	: : : : :	:: : : :	: : :	: : :	:
MM2	SLHIS-QYYFMPSCNYQ-YPVIIH-LIWMYGTIFFILFSNFWYHSYTKGKRLLPRAVQQNG					
	160	170	180	190	200	

GLELO	310
	AKEKARKLQ
MM2	APATTKVKAN
	210

FIG. 36

GLELO	50	60	70	80	90	100
AI225632	PTIVHTRGELVAVESPLARELPLMNP	FHVLLIVLAYLVTVFVGMQIMKNFERFEVKTF				
			::::: : : : : :			
	NEVNAFLDNMFGPRDSRVRGWFL	LD	SYLPTFFIL	TT	YLLSIWLG	KNKMRPALSLRGIL
	10	20	30	40	50	60
GLELO	110	120	130	140	150	160
AI225632	LLHNFCLV	SISAYMCGGILY	EAYQANYGLF	ENAAADHTFKG--L	PM	AK-MIWL
	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :
	TLYNLAITLL	SAYMLVELIL	SSWEGGYNL	QCQNLD	SAGEG	DVRVAKVLVW-YYFSKLVEF
	70	80	90	100	110	120
GLELO	170	180	190	200	210	220
AI225632	VDTMIMVL	KKNNRQISFL	HVYHHSSIFTI	WWLVTFVAPNGEAYFSAALNSFIHVIMYGY		
	: : : : :	: : : : :	: : : : :	: : : : :		
	LDTIFFVL	RKKANQITFL	HVYHHASMFNI			
	130	140	150			

FIG.37

20 30 40 50 60 70
 FMDLATAIGVRAAPYVDPLEAALVAQAEKYIPTIVHHTRGFLVAVESPLAREL-----PL

: | :: : | : : : | : | :
 MDTSMNFSRGLKMDLMQPYDFETFQDLRPF
 10 20 30

GLELO

U97107

80 90 100 110 120 129
 MNPFHV--LLIVLAYLVTVFGMQIMKNFERFEVKTFSLHNFCLVLSISAYMCGGILYEA
 :: : | : ||| :: || : || : | :: : | : | : | : | : | : | :
 LEEYVWSSFLIVVVYLLLVVGGQTYMRTRKSFSLQRPILWSEFFLAIFS--ILGTLRMWK
 40 50 60 70 80

GLELO

U97107

130 140 150 160 170 180
 YQAN----YGLFENAADHTFKGLPMAKMIW--LFYFSKIMEFVDTMIMVLKKNRQISFL
 :: | : | : : : : | : | : | : | : | : | : | : | : | :
 FMATVMFTVGLKQTVCFAIYTD DAVVRF-WSFLFLLSKVVELGDTAFIILRK--RPLIFV
 90 100 110 120 130 140

GLELO

U97107

FIG.38A

GLELO	190	200	210	220	230	240
	HVVHHSSI--FTIWWLVTFVAPNGEAYFSAALNSFIHVIMYGYFFLSALGFKQVSFIKFY					
			:	:	:	:
		:	:	:	:	:
U97107	150	160	170	180	190	200
	HWYHHSTVLLFTSFGYKNKV-PSGGWFMT--MNFVHVSVMYTYTMTKAAKLKHPNLLPMV					
GLELO	250	260	270	280	290	
	ITRSQMTQFCMMSVQSSWDMYAMKVLG--RPGYPFFITALLWFYMWMTMLGLFYN--FYRK					
		:	: : :	: :	: :	: :
		:	: : :	: :	: :	: :
U97107	210	220	230	240	250	260
	ITSLQILQMVLGTIFGILNYIWRQEKGCHTTTEHFFWSFMLYGTYFILFAHFFHRAYLRP					
GLELO	300	310				
	NAKLAKQAKADAAKEKARKLQ					
	: :	: : : :				
U97107	270					
	KGKVASKSQ					

FIG.38B

GLELO	60	70	80	90	100	110
	TRGFLVAVESPLARELPLMNP	FHLLIVLAYLVT	FVGMQIMKNFERFEVKT	FSLLHNFC		
		: :	: :	: :	: :	: :
U68749	30	40	50	60	70	80
(F56H11.4)	ATHGPKNFDAEGRKFFADHFDVT	IQASILYMVVFGTKWFMRNRQ	PFQLT	TIPLNIWNFI		
GLELO	120	130	140	150	160	
	LVSISAYMCGGILYEAYQ--	ANYGL--	FENAADHTFKGLPMAKMIWL	FYSKIMEFVDT		
	::	: :	: :	: :	: :	: :
U68749	90	100	110	120	130	140
(F56H11.4)	LAAFSIAGAVKMTPEFFGT	IANKGIVASYCKVDFDT-KG-	ENGYVWVLFMA	SKLFE	LVD	DT
GLELO	170	180	190	200	210	220
	MIMVLKNNRQISFLHVYHSSIFT	IWWLTVFAPNGEAYFSAALNSFI	HVIMYGYFLS			
	:: :	: :	: :	: :	: :	: :
U68749	150	160	170	180	190	
(F56H11.4)	IFVLRLK--RPLMFLHWYHIL	TMIYAWYSHPLTP-GFNRYGIY	LVNFVHAFMYSYFLR			
GLELO	230	240	250	260	270	280
	ALGFKQVSFIKFYITRSQMTQ	FCMMSVQSSWDMYAMKVLGRP-	GYPFFITALLWFYMWITM			
	: :	: :	: :	: :	: :	: :
U68749	200	210	220	230	240	250
(F56H11.4)	SMKIRVPGFIAQAITS	QIVQFIISCAVLAHLGYLMHFT	NANCDFEPSVFKLA	VFMDTTY		
GLELO	290	300	310			
	LGLFYNFYRKNAKLAKQAKA	DAKEKARKLQ				
	:	:	:			
U68749						
(F56H11.4)	260	270	280			
	LALFVNFFLQSYVLRG	GKDKYKAVPKKNN				

FIG.39

MAELO	10	20	30	40	50	59
	MAAAILDKNFGIDQPFGIKLDITYFAQAYELVTGKSIDSFVFQEGVTPPLSTQREVAMW-T					
U68749	::: : : : : : : : : : : : : :					
(F56H11.4)	MAQHPLVQRLILDVKFDT---KRFVAIAATHGPKNFPDAEGRKFFADHFDVTIQAS					
	10	20	30	40	50	
MAELO	60	70	80	90	100	110
	ITYFVVFGRQIMKSQDAFKLK-PLFILHNFLLTIASGSLLLFIENLVPILARNGLFY					
U68749	: : : : : : : : : : : : : : :					
(F56H11.4)	ILYMVVVFGTKWFMRNRQPFQLTIPLNIW-NFILAAFSIAGAVKMTPEFFGTIANKGIVA					
	60	70	80	90	100	110
MAELO	120	130	140	150	160	170
	AICDDGAWTQRLLELLYYLNYLV-KYWELADTVFLVLKKKPLEFLHYFHHMTMVLCFVQL					
U68749	: : : : : : : : : : : : : : : :					
(F56H11.4)	SYCKVFDEFTKGENGYWVWLFMASKLFELVDITIFLVLRRKRPLMFLHWYHHILTMIIYAWYSH					
	120	130	140	150	160	170

FIG.40A

MAELO 180 190 200 210 220 230
 GGYTSVSWVPITLNLTVHVEMY-YYMRSAAGVRI--WWKQYLTLQIVQFVLDLGFIFY
 : : ||::||:||||::||: :|:|:|||||::: : :
 U68749 PLTPGFNRYGIYLNFFVHAFMYSYFLRSMK-IRVPGFIAQAITSQIVQFIISCAVLAH
 (F56H11.4) 180 190 200 210 220

MAELO 240 250 260 270 280
 CAYT-YFAFTYFPWAPNVGKCAGTEGAALFGCGLLSSYLLLFINFYRITY-----NAKAK
 :| :|: : :|:| :| : :||| :|:|: :| :|
 U68749 LGYLMHFTNANCDFEPSVEKLA-----VF---MDTTYLALFVNFFLQSYVLRGGKDKYK
 (F56H11.4) 230 240 250 260 270 280

MAELO 290 300 310
 AAKERGSNFTPKTVKSGGSPKKPSKSKHI
 |: :: :|
 U68749 AVPKKKNN
 (F56H11.4)

FIG.40B

GLELO 40 50 60 70 80 90
AALVAQAEKYIPTIVHHTRGFLVAVESPLARELP LMNPFHVL LVLAYLVTVFVGMQIMK
| : | | | : | : : : | : : : | :
DM1 PTKMINMDISVTPNYSYIFDFENDFIHQRTTRKWMLENWTWVFYCYGIMLVIFGGQHFMQ
10 20 30 40 50 60

GLELO 100 110 120 130 140 150
NFERFEVKTFSLLHNFCLVSI SAYMCGGILYEAYQA--NYGLFENAADHTF--KGLPMAK
| | : : : | : : : | : : : | : : : | : : :
DM1 NRPRFQLRGPLIIWNTLLAMFSIMGAARTAPELIHVL RHYGLFHSVCVPSYIEQDRVC GF
70 80 90 100 110 120

GLELO 160 170 180 190 200 210
MIWLFYFSKIMEFVDTMIMVLKKNRQISFLHVYHHSSIFTIWWLVTVFVAPNGEAYFSAA
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DM1 WTWLFVLSKLP ELGDTIFIVLRK--QPLIFLHWYHHITVLIYSWF-SYTEYTS SARWFIV
130 140 150 160 170 180

GLELO 220 230 240 250 260 270
LNSFIHVIMYGYFLSALGFKQVSFIKFYITRSQMTQFCMMSVQSSWDMYAMKVLGRPGY
: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DM1 MNYCVHSVMSYSYALKAARFNPPRFISMIITSLQLAQMIIGCAINVWANGFLKTHGTXSC
190 200 210 220 230 240

GLELO 280 290 300 310
PFFITALLWFYMWMTMLGLFYNFYRKNAKLAKQAKADAAKEKARKLQ

DM1 HISQRNINLSIAMYSSYFVLFARFFYKAYLAPGGHKSRMA
250 260 270 280

FIG.41

MAELO	40	50	60	70	80	90
	VTGKSIDSFVFQEGVTPLSTQREVAMWTITYFVIFGGRQIMKSQDAFKLPFLILHNFL					
DM1	30	40	50	60	70	80
	IFDFENDFIHQTRKWKMLENWTWVFYCGIYMLVIFGGQHFMONRPRFQLRGPLIIWNTL					
MAELO	100	110	120	130	140	149
	LTIASGSLLLFIENLVPILARNGLFYAICDDGAWTQ--RLELLY--YLNVLVKYWELADTV					
DM1	90	100	110	120	130	140
	LAMFSIMGAARTAPELIHVLRHYGLFHSVCVPSYIEQDRVCVGFWTWLFVLSKLPGLGDTI					
MAELO	150	160	170	180	190	200
	FLVLKKKPLEFLHVFHHSMTMVLFCVQLGGYTS-VSWVPITLNLTVHVFMYYYMRSAAG					
DM1	150	160	170	180	190	200
	FIVLRKQPLIFLHWYHHITVLIYSWFSYTEYTSARWF-IVMNYCVHSMYSYYALKAAAR					
MAELO	210	220	230	240	250	260
	VRI--WWKQYLTTLQIVQFVLDLGFIFYFCAYTYFAFYFPWAPNVGKCAGTEGAALFGCG					
DM1	210	220	230	240	250	260
	FNPFRFISMIITSLQLAQMIIG-----CAINVWANGFLK-THGTXSCHISQORNINLSIA					
MAELO	270	280	290	300	310	
	LLSSYLLLFIFYRITYNAKAKAAKERGSNFTPKTVKSGGSPKPKPSKSKI					
DM1	260	270	280			
	MYSSYFVLFARFFYKAYLAPGGHKSRMA					

FIG.42

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1  ATGGAACATT TTGATGCATC ACTTAGTACC TATTTCAAGG CATTGCTAGG
51  CCTTCGAGAT ACTAGAGTAA AAGGATGGTT TCTTCTGGAC AATTATATAC
101 CCACATTTAT CTGCTCTGTC ATATATTTAC TAATTGTATG GCTGGGACCA
151 AAATACATGA GGAATAAACA GCCATTCTCT TGCCGGGGGA TTTTAGTGGT
201 GTATAACCTT GGAATCACAC TGCTGTCTCT GTATATGTTT TGTGAGTTAG
251 TAAACAGGAGT ATGGGAAGGC AAATACAACT TCTTCTGTCA GGCACACGC
301 ACCGCAGGAG AATCAGATAT GAAGATTATC CGTGTCCCTT GGTGGTACTA
351 CTTCTCCAAA CTCATAGAAAT TTATGGACAC TTTCTTCTTC ATCCTGCGCA
401 AGAACAAACCA CCAGATCACG GTCCTGCACG TCTACCACCA TGCCTCGATG
451 CTGAACATCT GGTGGTTTGT GATGAACTGG GTCCCCCTGG GCCACTCTTA
501 TTTTGGTGCC ACACTTAATA GCTTCATCCA CGTCCCTCATG TACTCTTACT
551 ATGGTTTGTC GTCAGTCCCT TCCATGCGTC CATACCTCTG GTGGAAGAAG
601 TACATCACTC AGGGCAGCT GCTTCAGTTT GTGCTGACAA TCATCCAGAC
651 CAGCTGCGGG GTCATCTGGC CGTGCACATT CCCTCTTGGT TGGTTGTATT
701 TCCAGATTGG ATACATGATT TCCCTGATTG CTCTCTTAC AACCTTCTAC
751 ATTCAGACCT ACAACAAGAA AGGGCCTCC CGAAGGAAAG ACCACCTGAA
801 GGACCACCAG AATGGGTCCA TGGCTGCTGT GAATGGACAC ACCAACAGCT
851 TTTCACCCCCT GGAATAACAAT GTGAAGCCAA GGAAGCTGGG GAAGGATTGA
901 AGTCAAAGAA TTGA

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FIG.43

1 MEHFDASLST YFKALLGPRD TRVKGWFLD NYIPTFICSV IYLLIVWLGP
51 KYMRNKQPFS CRGILVVYNL GLTLLSLYMF CELVTGVWEG KYNFFCQGTR
101 TAGESDMKII RVLWWYYFSK LIEFMDTFFF ILRKNNHQIT VLVVYHHASM
151 LNIWWFVMNW VPCGHSYFGA TLNSFIHVLN YSYYGGLSSVP SMRPYLWKKK
201 YITQGQLLQF VLTIIQTSCG VIWPCTFFPLG WLYFQIGYMI SLIALFTNFY
251 IQTYNKKGAS RRKDHCLKDHQ NGSMAAVNGH TNSFSPLENN VKPRKLKRD*

FIG.44

Host (plasmid)	334(pYX242)	334(pRAE-58-A1)	334(pYX242)	334(pRAE-58-A1)
Added substrate	25 μ M GLA	25 μ M GLA	25 μ M AA	25 μ M AA
Fatty acid	%total fatty acid	%total fatty acid	%total fatty acid	%total fatty acid
C18:3n-6	4.40	2.71	0.03	0.04
C20:3n-6	0.09	(50.34%)* 2.75	0.02	0.02
C20:4n-6			7.84	3.97
C22:4n-6			ND	(23.37%)* 1.21
C16:1n-7	41.11	34.72	41.49	35.07
C18:1n-7	1.85	11.33	2.01	11.57
C20:1n-7	0.04	1.48	0.04	1.62
C18:1n-9	15.60	15.66	15.16	14.57
C20:1n-9	0.06	0.22	0.06	0.23
C18:1n-5	0.11	0.62	0.12	0.58
Total Lipid	370	969	359	514
*% conversion=product/(substrate+product)				

FIG.45

1 ATGGCTCAGC ATCCGCTCGT TCAACGGCTT CTCGATGTCA AATTCGACAC
51 GAAACGATTT GTGGCTATTG CTACTCATGG GCCAAAGAAT TTCCCTGACG
101 CAGAAGGTGG CAAGTTCTTT GCTGATCACT TTGATGTTAC TATTCAGGCT
151 TCAATCCTGT ACATGGTCGT TGTGTCGGA ACAAAATGGT TCATGCGTAA
201 TCGTCAACCA TTCCAATTGA CTATTCCACT CAACATCTGG AATTCATCC
251 TCGCCGCATT TTCCATCGCA GGAGCTGTCA AAATGACCCC AGAGTTCCTT
301 GGAACCATTT CCAACAAGG AATTGTCGCA TCCTACTGCA AAGTGTTTGA
351 TTTCACGAAA GGAGAGAAATG GATACTGGGT GTGGCTCTTC ATGGCTTCCA
401 AACTTTTCGA ACTTGTGAC ACCATCTTCT TGGTTCCTCG TAAACGTCCA
451 CTCATGTTCC TTCACTGGTA TCACCATATT CTCACCATGA TCTACGCCCTG
501 GTACTCTCAT CCATTGACCC CAGGATTCAA CAGATACGGA ATTTATCTTA
551 ACTTTGTCGT CCACGCCCTC ATGTACTCTT ACTACTTCCT TCGCTCGATG
601 AAGATTCGGG TGCCAGGATT CATCGCCCAA GCTATCACAT CTCCTTCAAAAT
651 CGTTCAATTC ATCATCTCTT GCGCCGTTCT TGCTCATCTT GGTATCTCA
701 TGCACCTCAC CAATGCCAAC TGTGATTTTG AGCCATCAGT ATTCAAGCTC
751 GCAGTTTTC TGGACACAAC ATACTTGGCT CTTTTCGTCA ACTTCTTCTT
801 CCAATCATAT GTTCTCCGGG GAGGAAAAGA CAAGTACAAG GCAGTGCCAA
851 AGAAGAAGAA CAACTAA

FIG.46

1 MAQHPLVQRL LDVKFDTKRF VAIATHGPKN FPDAEGRKFF ADHFDVVTIQA
51 SILYMVVVFG TKWFMRNRQP FQLTIPLNIW NFILAAFSIA GAVKMTPEFF
101 GTIANKGIVA SYCKVFDEFTK GENGYWVWLF MASKLFELVD TIFLVLRKRP
151 LMFLHWYHHI LTMIIYAWYSH PLTPGFNRYG IYLNFFVVHAF MYSYYFLRSM
201 KIRVPGFIAQ AITSLQIVQF IISCAVLAHL GYLMHFTNAN CDFEPSVFKL
251 AVFMDTTYLA LEVNFFLQSY VLRGGKDKYK AVPKKKNN

FIG.47

Host (plasmid)	334(pYX242)	334(pRET-21)	334(pRET-22)
Added Substrates	50 μ M GLA + 50 μ M AA	50 μ M GLA + 50 μ M AA	50 μ M GLA + 50 μ M AA
Fatty Acid	%total fatty acid	%total fatty acid	%total fatty acid
C16:0	9.22	12.46	9.9
C16:1	0.09	0.18	0.13
C18:0	1.46	2.41	1.49
C18:1n-9	4.03	4.92	3.91
C18:3n-6	10.02	11.89	8.69
C20:3n-6	(1.28%)* 0.13	(11.1%)* 1.48	(19.4%)* 2.09
C20:4n-6	46.98	28.87	35.25
C22:4n-6	0	0	0
Total lipid (mg)	212	174	187
*% conversion=product/(substrate+product)			

FIG.48

```

1  ATGAACATGT CAGTGTGAC TTTACAAGAA TATGAATTCTG AAAAGCAGTT
51  CAACGAGAAAT GAAGCCATCC AATGGATGCA GGAAACTGG AAGAAATCTT
101 TCCTGTTTTC TGCTCTGTAT GCTGCCTTTA TATTCGGTG TCGGCACCTA
151 ATGAATAAAC GAGCAAAAGTT TGAAC TGAGG AAGCCATTAG TGCTCTGTC
201 TCTGACCCCTT GCAGTCTTCA GTATAATTCGG TGCTCTTCA ACTGGTGCTT
251 ATATGGTGTA CATTTTGATG ACCAAAGGCC TGAAGCAGTC AGTTTGTGAC
301 CAGGGTTTTT ACAATGGACC TGTCAGCAAA TTCTGGGCTT ATGCATTTGT
351 GCTAAGCAAA GCACCCGAAC TAGGAGATAC AATATTCAAT ATCTGAGGA
401 AGCAGAAGCT GATCTTCCTG CACTGGTATC ACCACATCAC TGTGCTCCTG
451 TACTCTTGGT ACTCCTACAA AGACATGGTT GCCGGGGAG GTTGGTTCAT
501 GACTATGAAC TATGGCGTGC ACGCCGTGAT GTACTCTTAC TATGCCCTGC
551 GGGCGGCAGG TTTCCGAGTC TCCCGGAAGT TTGCCATGTT CATCACCTTG
601 TCCCAGATCA CTCAGATGCT GATGGGCTGT GTGGTTAACT ACCTGGTCTT
651 CTGCTGGATG CAGCATGACC AGTGTCACCTC TCACCTTTCAG AACATCTTCT
701 GGTCCCTCACT CATGTACCTC AGCTACCTTG TGCTCTCTG CCATTTCTTC
751 TTTGAGGCCT ACATCGGCAA AATGAGGAAA ACAACGAAAG CTGAATAG

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FIG.49

1 MNMSVLTQEQEYEFKQFNEN EAIQWMQENW KKSFLFSALY AAFIFGGRHL
51 MNKRAKFEIR KPLVLWLSLTL AVFSIFGALR TGAYMVYILM TKGLKQSVCD
101 QGFYNGPVSF FWAYAFVLSK APELGDTIFI ILRKQKLIFL HWYHHITVLL
151 YSWYSYKDMV AGGGWFMTMN YGVHAVMYSY YALRAAGFRV SRKFAMFITL
201 SQITQMLMGC VVNYLVFCWM QHDQCHSHFQ NIFWSSLMYL SYLVLFCHFF
251 FEAYIGKMRK TTKAE*

FIG.50

Host	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334
Plasmid	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pYX242	pYX242	pYX242	pYX242	pYX242	pYX242	pRAE-58
Substrate	GLA	GLA	AA	AA	AA	AA	STA	STA	STA	STA	STA	EPA	EPA	EPA	OA	ALA	ALA	ALA
Concentration	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M
% total lipid																		
C18:1n-9	18.75	12.96	16.95	12.76	16.06	14.18	19.55	13.78	29.42	23.06	ND	14.58						
C18:1n-7	2.00	18.49	2.30	18.70	1.45	13.26	2.75	13.62	2.50	16.42	1.87	13.76						
C18:1n-5	0.29	1.63	0.24	1.61	0.33	0.97	0.32	1.10	0.30	1.64	0.28	1.18						
C18:3n-6	4.61	2.02	0.04	0.04	0.02	0.09	0.06	0.05	0.02	0.05	0.01	0.01						
C18:3n-3	0.02	0.08	0.02	0.07	0.01	0.03	0.04	0.05	0.02	0.08	14.74	14.08						
C18:4n-3	ND	ND	ND	ND	7.01	2.65	ND	ND	ND	ND	ND	ND						
C20:1n-9	0.10	0.77	0.11	0.70	0.15	0.55	0.15	0.46	0.27	2.25	0.10	0.57						
C20:1n-7	0.08	8.45	0.10	8.06	0.04	3.95	0.14	4.48	0.10	(8.9%)9.35	0.06	3.53						
C20:3n-6	0.17	(78.3%)7.29	0.01	0.07	ND	0.04	ND	ND	ND	ND	ND	ND						
C20:3n-3	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND						
C20:4n-6	ND	ND	22.07	8.40	ND	0.07	ND	ND	ND	ND	ND	ND						
C20:4n-3	ND	ND	ND	ND	0.25	(79.2%)10.07	ND	ND	ND	ND	ND	ND						
C20:5n-3	ND	ND	0.01	ND	0.18	0.08	8.21	2.63	ND	0.02	ND	ND						
C22:4n-6	ND	ND	ND	(42.7%)6.26	ND	ND	ND	ND	ND	ND	ND	ND						
C22:5n-3	ND	ND	ND	ND	ND	0.18	ND	(71.7%)6.66	ND	ND	ND	ND						
Total Lipid	158	104	144	112	324	209	178	94	148	87	243	315						

(% conversion) = product/(substrate + product)
 ND = not detected

FIG.51

Host	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334
Plasmid	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pRAE-58
Substrate	GLA	GLA	GLA	GLA	GLA	GLA	GLA	GLA	GLA	GLA	GLA	GLA	GLA	GLA	GLA	GLA	EPA
Concentration	25 μ M	25 μ M	100 μ M	100 μ M	25 μ M	25 μ M	25 μ M	25 μ M	100 μ M	100 μ M	25 μ M	25 μ M	100 μ M	25 μ M	25 μ M	100 μ M	100 μ M
% total lipid																	
C18:1n-9	23.82	21.49	18.49	17.41	22.09	19.23	17.45	18.44	24.78	21.28	19.42	18.85					
C18:1n-7	2.52	18.35	1.71	11.82	2.54	18.77	1.78	12.67	2.64	19.48	1.79	12.40					
C18:1n-5	0.15	1.13	0.10	0.54	0.15	1.23	0.10	0.63	0.15	1.18	0.09	0.62					
C18:3n-6	6.10	2.38	23.30	14.46	0.04	0.02	0.04	0.02	0.04	0.02	0.01	0.01					
C20:1n-9	0.08	0.83	0.05	0.48	0.10	1.18	0.04	0.56	0.10	1.30	0.06	0.63					
C20:1n-7	0.10	5.75	0.07	3.09	0.11	9.49	0.05	3.62	0.10	9.94	0.08	4.07					
C20:3n-6	0.15	(62.4%)3.95	0.31	(39.8%)9.56	0.02	ND	ND	0.04	ND	0.02	0.01	0.01					
C20:4n-6	ND	ND	0.01	ND	11.76	7.68	28.39	21.02	0.02	0.02	ND	0.01					
C20:5n-3	ND	ND	ND	ND	0.03	0.02	0.10	0.07	4.79	2.04	26.47	13.69					
C22:4n-6	ND	ND	ND	ND	ND	(27.5%)2.91	0.01	(15.7%)3.90	ND	ND	0.00	ND					
C22:5n-3	ND	ND	ND	ND	ND	ND	ND	0.03	0.02	(70.3%)4.82	0.04	(45.7%)11.50					
Total Lipid	230	419	590	576	249	332	1014	961	372	390	1323	1065					

(% conversion) = product/(substrate + product)
 ND = not detected

FIG.52

Host	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334
Plasmid	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242
Substrate	PA	PA	SA	SA	ARA	ARA	ARA	ARA	BA	BA	PTA	PTA	PTA	PTA	OA	OA	OA	EA	EA
Concentration	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M
% total lipid																			
C16:0	24.17	17.23	11.22	7.90	7.74	7.98	7.98	7.62	7.11	17.28	11.04	16.06	12.76	14.37	11.98				
C16:1n-7	39.83	33.83	30.62	20.56	21.61	19.81	21.34	22.89	22.89	50.06	39.43	40.95	30.06	43.34	29.51				
C16:1n-5	0.30	0.74	0.29	0.58	0.17	0.47	0.18	0.59	0.59	0.38	0.80	0.34	0.68	0.37	0.71				
C18:0	1.90	1.50	35.82	38.10	1.12	0.89	1.03	0.88	0.88	1.90	1.44	1.82	1.43	1.51	1.23				
C18:1n-9	15.36	14.11	11.52	10.88	8.29	10.03	8.09	10.25	10.25	14.55	13.86	20.12	21.37	14.12	15.15				
C18:1n-7	1.36	11.44	0.90	8.72	0.69	8.51	0.69	8.58	8.58	1.30	12.76	1.30	13.79	1.21	12.66				
C18:1n-5	0.11	0.78	0.08	0.69	0.08	0.54	0.06	0.61	0.61	0.19	0.76	0.10	0.90	0.15	0.84				
C20:0	0.15	0.17	0.09	0.12	52.07	41.48	ND	ND	ND	ND	ND	ND	ND	0.17	0.23				
C20:1n-9	0.09	0.45	0.05	0.30	0.03	ND	0.06	0.28	0.28	0.05	0.38	0.18	0.58	7.47	10.97				
C20:1n-7	0.20	2.84	ND	1.52	0.05	1.43	0.14	1.60	1.60	0.07	2.76	0.12	2.08	ND	2.30				
C22:0	0.43	0.56	0.29	0.22	0.31	0.19	52.91	38.43	38.43	ND	ND	ND	ND	ND	0.32				
C24:0	0.59	1.39	0.36	0.85	0.45	0.71	0.53	1.14	1.14	0.45	1.63	0.66	1.02	0.56	0.79				
Total Lipid	297	272	573	542	558	846	585	519	464	295	306	448	309	648					

ND = not detected

FIG.53A

Host	334	334	334	334	334	334	334	334	334	334	334	334	334
Plasmid	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pRAE-58	pYX242	pYX242	pRAE-58
Substrate	LA	LA	GLA	GLA	DGLA	DGLA	DGLA	DGLA	AA	AA	AA	ADA	ADA
Concentration	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M
% total lipid													
C18:1n-9	15.27	16.83	14.85	15.58	13.62	16.24	15.08	15.64	16.18	13.98			
C18:1n-7	1.21	13.53	1.22	11.80	1.16	12.63	1.18	11.70	1.30	10.67			
C18:1n-5	0.13	0.95	0.20	0.73	0.12	0.72	0.14	0.59	0.12	0.70			
C18:2n-6	4.09	4.85	0.09	0.07	0.07	0.04	0.04	0.04	0.03	0.07			
C18:3n-6	ND	ND	4.66	2.33	ND	ND	ND	ND	ND	ND			
C20:1n-9	0.07	2.60	0.07	0.33	0.07	0.33	0.04	0.27	0.08	0.33			
C20:1n-7	0.10	0.18	0.14	1.65	0.08	1.68	0.12	1.58	0.12	1.85			
C20:2n-6	ND	(13.2%)0.74	ND	ND	ND	ND	ND	ND	ND	ND			
C20:3n-6	ND	ND	ND	(51.4%)2.46	6.37	7.86	ND	0.03	ND	ND			
C20:4n-6	ND	ND	ND	ND	ND	0.09	6.49	5.77	ND	ND			
C22:4n-6	ND	ND	ND	ND	ND	ND	ND	(27.1%)2.14	10.91	15.57			
C24:0	0.59	1.61	0.64	1.12	0.69	0.79	0.52	0.77	0.54	1.26			
Total Lipid	333	373	260	392	260	672	553	690	706	440			

(% conversion) = product/(substrate + product)

ND = not detected

FIG.53B

Host	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334
Plasmid	pYX242	pRAE-58	pYX242	pYX242	pRAE-58	pYX242	pYX242	pRAE-58	pYX242	pYX242	pRAE-58	pYX242	pYX242	pRAE-58	pYX242	pYX242	pRAE-58
Substrate	ALA	ALA	STA	STA	STA	STA	STA	STA	STA	STA	STA	STA	STA	STA	STA	STA	STA
Concentration	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M
% total lipid																	
C18:1n-9	17.21	17.36	16.85	17.71	16.45	16.93	17.08	16.68	18.36	18.77							
C18:1n-7	1.29	12.20	1.15	11.38	1.23	11.48	1.33	11.61	1.46	13.72							
C18:1n-5	0.14	0.68	0.12	0.57	0.12	0.54	0.12	0.63	0.13	0.79							
C18:3n-3	4.42	3.61	ND	0.03	ND	0.03	ND	0.03	ND	0.03							
C18:4n-3	ND	0.13	3.04	1.38	ND	0.13	ND	0.13	ND	0.17							
C20:1n-9	0.09	0.33	0.11	0.34	0.05	0.31	0.09	0.30	0.13	0.34							
C20:1n-7	0.13	1.55	0.05	1.38	0.23	1.89	0.18	1.73	0.15	1.76							
C20:3n-3	0.06	(22.2%)1.03	ND	ND	ND	0.11	ND	ND	ND	ND							
C20:4n-3	ND	ND	0.06	(61.9%)2.24	ND	ND	ND	ND	ND	ND							
C20:5n-3	ND	ND	0.05	0.05	7.43	4.88	ND	ND	0.07	ND							
C22:4n-3	ND	ND	ND	0.39	ND	ND	ND	ND	ND	ND							
C22:5n-6	ND	ND	ND	ND	ND	ND	0.28	0.41	ND	ND							
C22:5n-3	ND	ND	ND	ND	ND	(39.5%)3.19	3.99	5.94	ND	ND							
C24:0	0.43	0.73	0.33	0.73	0.45	0.84	0.64	1.07	0.68	0.77							
C24:5n-3	ND	ND	ND	ND	ND	0.08	ND	0.06		ND							
Total Lipid	696	729	911	710	719	703	602	642	397	684							

(% conversion) = product/(substrate + product)

ND = not detected

FIG.53C

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1 ATGGAGCAGC TGAAGGCCTT TGATAATGAA GTCAATGCTT TCTTGGACAA
51 CATGTTTGGA CCACGAGATT CTCGAGTTCG CGGGTGGTTC CTGCTGGACT
101 CTTACCTTCC CACCTTCATC CTCACCATCA CGTACCTGCT CTCGATATGG
151 CTGGGTAACA AGTACATGAA GAACAGGCCT GCTCTGTCTC TCAGGGGCAT
201 CCTCACCTTG TATAACCTCG CAATCACACT TCTTTCTGCG TATATGCTGG
251 TGGAGCTCAT CCTCTCCAGC TGGGAAGGAG GTTACAACCTT GCAGTGTGAG
301 AATCTCGACA GTGCAGGAGA AGGTGATGTC CGGGTAGCCA AGGTCTTGTG
351 GTGGTACTAC TTCTCCAAAC TAGTGGAGTT CCTGGACACG ATTTTCTTTG
401 TTCTACGAAA AAAGACCAAT CAGATCACCT TCCTTCATGT CTATCACCAC
451 GCGTCCATGT TCAACATCTG GTGGTGTGTT TTGAACTGGA TACCTTGTGG
501 TCAAAGCTTC TTTGGACCCA CCCTGAACAG CTTTATCCAC ATTCTCATGT
551 ACTCCTACTA CGGCCTGTCT GTGTTCCCGT CCATGCACAA GTACCTTTGG
601 TGGAAGAAGT ACCTCACACA GGCTCAGCTG GTGCAGTTCG TACTCACCAT
651 CACGCACACG CTGAGTGCCG TGGTGAAGCC CTGTGGCTTC CCCTTTGGCT
701 GTCTCATCTT CCAGTCTTCC TATATGATGA CGCTGGTCAT CCTGTTCTTA
751 AACTTCTATA TTCAGACATA CCGGAAAAAG CCAGTGAAGA AAGAGCTGCA
801 AGAGAAAGAA GTGAAGAATG GTTCCCCAA AGCCCACTTA ATTGTGGCTA
851 ATGGCATGAC GGACAAGAAG GCTCAATAA

FIG.54

1 MEQLKAFDNE VNAFLDNMFG PRDSRVRGWF LLDSYLPFI LTITYLLSIW
51 LGNKYMKNRP ALSLRGILT YNLAITLLSA YMLVELILSS WEGGYNLQCQ
101 NLDSAGEGDV RVAKVLWYY FSKLVEFLDT IFFVLRKKTN QITFLHVVHH
151 ASMFIWWCV LNWIPCGQSF FGPTLNSFIH ILMYSYYGLS VFPSMHKYLW
201 WKKYLTQAQL VQFVLTITHT LSAVVKPCGF PFGCLIFQSS YMMTLVILFL
251 NFYIQTYRKK PVKKELQEKE VKNGFPAHL IVANGMTDKK AQ*

FIG.55

Host	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334
Plasmid	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pRAE-84
Substrate	GLA	GLA	AA	AA	ADA	ADA	ADA	ADA	ADA	ADA	ADA	ADA	ADA	ADA	ADA	ADA	ADA	ADA	DPA
Concentration	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM	25μM
% total lipid																			
C18:1N-9	15.94	14.16	12.30	15.67	11.77	11.41	14.81	17.92	15.91	16.33	15.04	14.63							
C18:1N-7	1.25	1.21	1.10	1.50	1.13	1.18	1.19	1.38	1.33	1.49	1.37	1.38							
C18:3N-6	4.53	4.21	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND							
C18:4N-3	ND	ND	ND	ND	ND	ND	2.78	2.70	ND	ND	ND	ND							
C20:1N-7	ND	ND	ND	ND	ND	0.32	ND	0.03	ND	0.05	ND	ND							
C20:3N-6	0.10	0.37	ND	ND	ND	ND	ND	0.05	ND	ND	ND	ND							
C20:4N-6	ND	ND	11.44	5.55	ND	ND	ND	ND	ND	ND	ND	ND							
C20:4N-3	ND	ND	ND	ND	ND	ND	ND	(14%)0.44	ND	ND	ND	ND							
C20:5N-3	ND	ND	ND	ND	ND	ND	ND	ND	9.68	3.02	ND	ND							
C22:4N-6	ND	ND	ND	(10.4%)0.64	20.41	23.61	ND	ND	ND	ND	ND	ND							
C22:4N-3	ND	ND	ND	ND	ND	ND	ND	(42.3%)0.33	ND	ND	0.57	0.57							
C22:5N-3	ND	ND	ND	ND	ND	ND	ND	ND	ND	(32.7%)1.47	7.87	4.88							
C24:4N-6	ND	ND	ND	(62.6%)1.07	ND	(9.2%)2.4	ND	ND	ND	ND	ND	ND							
C24:5N-3	ND	ND	ND	ND	ND	ND	ND	ND	ND	(82.8%)7.06	ND	(43.9%)3.82							
Total Lipid	208	126	115	189	158	149	124	433	221	271	127	126							

(% conversion) = product/(substrate + product)

ND = not detected

FIG.56

Host	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334
Plasmid	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pRAE-84
Substrate	PA	PA	SA	SA	ARA	ARA	BA	BA	PTA	PTA	PTA	PTA	PTA	PTA	PTA	PTA	PTA	PTA	PTA	PTA	PTA
Concentration	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M
% total lipid																					
C16:0	36.30	39.95	7.12	8.31	5.78	4.42	4.17	5.76	18.69	18.85	14.69	18.91	15.25	18.88							
C16:1n-7	26.22	23.52	11.77	15.25	10.23	6.29	7.01	10.10	38.48	41.23	20.55	31.48	25.89	40.32							
C16:1n-5	0.23	0.28	0.16	0.20	0.13	0.07	0.09	0.13	0.38	0.38	0.26	0.43	0.35	0.41							
C18:0	2.26	2.14	64.90	58.73	0.94	1.01	0.64	0.85	2.17	2.29	3.02	2.73	2.71	2.15							
C18:1n-9	14.83	11.27	6.35	7.22	5.20	4.33	3.84	5.12	14.25	14.27	18.44	22.20	14.62	16.91							
C18:1n-7	1.44	1.36	0.57	0.73	0.54	0.51	0.41	0.56	1.57	1.68	1.53	1.67	1.65	1.84							
C18:1n-5	0.10	ND	ND	0.06	ND	ND	ND	0.06	0.17	0.15	ND	0.18	ND	0.16							
C20:0	0.59	0.24	0.09	0.08	66.40	74.78	0.10	0.05	0.17	0.17	0.24	0.20	0.33	0.04							
C20:1n-9	0.06	0.10	ND	0.04	0.05	0.06	ND	ND	ND	ND	0.25	0.16	13.15	7.07							
C20:1n-7	0.07	ND	ND	ND	ND	0.12	ND	ND	ND	ND	0.40	ND	ND	0.04							
C22:0	0.45	0.75	0.29	0.30	0.43	0.31	77.35	70.71	0.74	0.80	0.98	0.74	0.83	0.44							
C24:0	0.55	1.09	0.38	0.41	0.69	0.62	0.50	0.45	0.94	0.92	1.67	0.96	ND	0.53							
Total Lipid	158	104	144	112	324	209	178	94	148	87	243	315	70	529							

ND = not detected

FIG.57A

Host	334	334	334	334	334	334	334	334	334	334	334	334
Plasmid	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pRAE-84	pYX242	pYX242	pYX242	pRAE-84
Substrate	LA	LA	GLA	GLA	DGLA	DGLA	AA	AA	AA	AA	ADA	ADA
Concentration	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M
% total lipid												
C18:1n-9	12.30	16.12	15.63	16.28	14.28	13.77	16.21	15.04	15.38	15.38	12.94	12.94
C18:1n-7	1.34	1.87	1.69	1.90	1.41	1.61	1.61	1.62	1.51	1.51	1.47	1.47
C18:2n-6	2.67	3.61	0.17	0.20	0.24	0.21	0.09	0.09	0.06	0.06	0.14	0.14
C18:3n-6	ND	ND	2.03	2.49	ND	ND	ND	ND	ND	ND	ND	ND
C20:3n-6	ND	ND	ND	(14.7%)0.43	10.59	10.73	ND	ND	ND	ND	ND	ND
C20:4n-6	ND	ND	ND	ND	ND	ND	14.03	5.27	ND	ND	ND	ND
C22:4n-6	ND	ND	ND	ND	ND	ND	ND	(8.7%)0.5	11.44	11.44	16.60	16.60
C24:0	0.79	1.00	1.08	1.16	1.30	0.87	0.87	0.72	0.77	0.77	1.18	1.18
C24:4n-6	ND	ND	ND	ND	ND	ND	ND	(43.8%)0.39	ND	ND	(7.3%)1.3	(7.3%)1.3
C24:5n-6	ND	ND	ND	ND	ND	ND	ND	0.38	ND	ND	ND	ND
Total Lipid	85	87	88	79	107	98	208	212	304	304	122	122

* % Conversion=product/(substrate + product)

ND=not detected

FIG.57B

Host	334	334	334	334	334	334	334	334	334	334	334	334	334
Plasmid	pXY242	pRAE-84	pYX242	STA	pRAE-84	pYX242	EPA	25 μ M	25 μ M	DPA	25 μ M	pYX242	pRAE-84
Substrate	ALA	ALA	STA	25 μ M	STA	25 μ M	EPA	25 μ M	DPA	25 μ M	25 μ M		
Concentration	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M	25 μ M		
% total lipid													
C18:1n-9	16.69	16.38	18.24	15.95	14.07	15.16	16.05	15.06	17.47	17.15			
C18:1n-7	1.37	1.43	1.71	1.40	1.37	1.47	1.67	1.51	1.75	1.73			
C18:2n-6	0.08	0.08	0.12	0.04	0.13	0.06	0.11	0.18	0.13	0.15			
C18:3n-3	4.47	4.28	ND	ND	ND	ND	ND	ND	ND	ND			
C18:4n-3	ND	ND	2.28	2.39	ND	ND	ND	ND	ND	ND			
C20:3n-3	(1.3%)0.06	(3.6%)0.16	ND	ND	ND	0.26	ND	ND	ND	0.12			
C20:4n-3	ND	ND	ND	(11.1%)0.3	ND	ND	ND	ND	ND	ND			
C20:5n-3	ND	0.07	ND	ND	9.97	3.84	ND	ND	ND	ND			
C22:4n-3	ND	ND	ND	(43.4%)0.23	ND	ND	ND	ND	ND	ND			
C22:5n-6	ND	ND	ND	ND	ND	ND	0.64	0.55	ND	ND			
C22:5n-3	ND	ND	ND	ND	ND	(24.0%)1.21	8.79	3.57	ND	ND			
C24:0	0.65	0.43	1.41	0.58	1.38	0.78	1.45	1.35	0.89	0.67			
C24:5n-3	ND	ND	ND	ND	ND	(73.6%)3.38	ND	(46.4%)3.09	ND	ND			
Total Lipid	362	384	173	393	124	280	137	151	190	200			

*% conversion = product/(substrate + product)

ND = not detected

FIG.57C

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1 ATGGAACATT TCGATGCGTC ACTCAGTACC TATTTCAAGG CCTTCCTGGG
51 CCCCCGAGAT ACAAGAGTCA AAGGATGGT CCTCCTGGAC AATTACATCC
101 CTACGTTTGT CTGTTCTGTT ATTTACTTAC TCATTGTATG GCTGGGACCA
151 AAATACATGA AGAACCGGCA GCCGTTCTCT TGCCGAGGCA TCCTGCAGTT
201 GTATAACCTT GGA CTCACCC TGCTGTCTCT CTACATGTTT TATGAGTTGG
251 TGACAGGTGT GTGGGAGGGC AAATACAAC TTTTCTGCCA GGGAAACACGC
301 AGCGCGGGAG AATCCGATAT GAAGATCATC CGCGTCCTCT GGTGGTACTA
351 CTTCTCCAAA CTCATCGAAT TCATGGACAC CTTTTTCTTC ATCCTTCGCA
401 AGAACAACCA CCAGATCACC GTGCTCCATG TCTACCACCA CGCTACCATG
451 CTCAACATCT GGTGGTTTGT GATGAACTGG GTTCCCTGCG GCCATTCATA
501 TTTTGGTGCG ACACTCAACA GCTTCATCCA TGTCTCATG TACTCGTACT
551 ATGGTCTGTC CTCCATCCCG TCCATGCGTC CCTACCTCTG GTGGAAAAAG
601 TACATCACTC AAGGGCAGCT GGTCCAGTTT GTGCTGACAA TCATCCAGAC
651 GACCTGCGGG GTCTTCTGGC CATGCTCCTT CCCTCTCGGG TGGCTGTTCT
701 TCCAGATTGG ATACATGATT TCCCTGATTG CTCTCTTAC AAATTCTAC
751 ATTCAGACTT ACAACAAGAA AGGGGCCTCT CGGAGGAAAG ACCACCTGAA
801 GGGCCACCAG AACGGGTCTG TGGCCGCCGT CAACGGACAC ACCAACAGCT
851 TCCCTTCCCT GGAAAAACAGC GTGAAGCCCA GGAAGCAGCG AAAGGATTGA
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FIG.58

```
1 MEHFDASLST YKFAFLGPRD TRVKGWFLLD NYIPTFVCSV IYLLIVWLGP
51 KYMKNRQPFS CRGILQLYNL GLTLLSLYMF YELVTGVWEG KYNFFCQGTR
101 SAGESDMKII RVLWYYYFSK LIEFMDTFFF ILRKNNHQIT VLVHYHHATM
151 LNIWWFVMNW VPCGHSYFGA TLNSFIHVLM YSYYGLSSIP SMRPYLWKK
201 YITQGQLVQF VLTIIQTTCG VFWPCSFPLG WLFFQIGYMI SLIALFTNFY
251 IQTYNKKGAS RRKDHLKGHQ NGSVAAVNGH TNSFPSLENS VKPRKQRKD*
```

FIG.59

Host	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334	334
Plasmid	pYX242	pRAE-87	pYX242	pRAE-87	pYX242	pRAE-87	pYX242	pRAE-87	pYX242	pRAE-87	pYX242	pRAE-87	pYX242	pRAE-87	pYX242	pRAE-87	pYX242	pRAE-87
Substrate	GLA	GLA	AA	AA	ADA	ADA	ADA	ADA	ADA	ADA	ADA	ADA	ADA	ADA	ADA	ADA	ADA	ADA
Concentration	25mM	25mM	25mM	25mM	25mM	25mM	25mM	25mM	25mM	25mM	25mM	25mM	25mM	25mM	25mM	25mM	25mM	25mM
% total lipid																		
C18:1n-9	15.94	12.05	12.30	12.61	11.77	10.91	14.81	15.52	15.91	16.66	15.04	8.07						
C18:1n-7	1.25	8.00	1.10	9.60	1.13	8.87	1.19	8.94	1.33	11.60	1.37	6.90						
C18:3n-6	4.53	1.11	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND						
C18:4n-3	ND	ND	ND	0.09	ND	0.14	2.78	0.80	ND	ND	ND	ND						
C20:1n-7	ND	0.98	ND	0.91	ND	0.63	ND	0.62	ND	0.94	ND	1.34						
C20:3n-6	0.10	(78.7%)4.1	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND						
C20:4n-6	ND	ND	11.44	11.28	ND	ND	ND	ND	ND	ND	ND	ND						
C20:4n-3	ND	ND	ND	ND	ND	ND	ND	(81.0%)3.4	ND	ND	ND	ND						
C20:5n-3	ND	ND	ND	ND	ND	ND	ND	ND	9.68	4.58	ND	ND						
C22:4n-6	ND	ND	ND	(36.0%)6.33	20.41	21.15	ND	ND	ND	ND	ND	ND						
C22:4n-3	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	0.57	ND						
C22:5n-3	ND	ND	ND	ND	ND	ND	ND	ND	ND	(57.4%)6.18	7.87	17.24						
C24:4n-6	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND						
C24:5n-3	ND	ND	ND	ND	ND	ND	ND	ND	ND	(4.2%)0.27	ND	(1.4%)0.25						
Total Lipid	208	102	115	177	158	117	124	200	221	199	127	91						

(% conversion) = product/(substrate + product)

ND = not detected

FIG.60

Host(plasmid)	334(pYX242)	334(pRET-22)	334(pYX242)	334(pRET-22)	334(pYX242)	334(pRET-22)
Added Substrates	50 mM GLA	50 mM GLA	50 mM AA	50 mM AA	no substrate	no substrate
% total lipid						
Fatty Acid						
C16:0	19.8	18.59	13.8	6.23	13.62	13.63
C16:1n-7	20.92	17.74	26.62	13.01	40.1	47.67
C18:0	5.79	4.94	3.62	2	4.86	5.031
C18:1n-7	(3.9%) 0.85	(9.12%) 1.78	(3.5%) 0.97	(12.54%) 1.18	(3.6%) 1.5	(7.53%) 3.88
C18:1n-9	8.46	7.45	10.27	5.36	13.7	16.93
C18:3n-6	*26.62	*22.03	0.03	0.01		
C20:3n-6	(1.1%) 0.3	(38.2%) 13.61				
C20:4n-6			*27.36	* 65.38		
C22:4n-6						
Total Lipid (μ g)	36	42	85	280	55	79
(% conversion) = product/(substrate + product)						
*indicates substrate added						

FIG.61

Host (plasmid)	334 (pRET22)	334 (pRET22)	334 (pRET22)	334 (pRET22)	334 (pRET22)	334 (pRET22)
Added Substrate	50 μ M SA	50 μ M OA	50 μ M LA	50 μ M DGLA	25 μ M AA	50 μ M Adrenic
	C18:0	C18:1n-9	C18:2n-6	C20:3n-6	C20:4n-6	C22:4n-6
Fatty Acid	%total lipid					
C16:0	12.9	12.54	15.23	9.1	10.2	3.42
C16:1	37.71	23.83	24.87	16.61	18.375	7.66
C18:0	11.44	4.7	4.49	2.7	2.9	1.23
C18:1n-9	14.03	*16.87	9.54	6.74	6.39	2.99
C18:2n-6			16.87		0.15	0.28
C18:3n-6						
C20:2n-6						0.05
C20:3n-6				*44.34		
C20:4n-6				0.34	*25.78	0.26
C22:4n-6						*75.72
Total Lipid (μ g)	63	103	71	110	97	277

*indicates substrate added
 (% conversion) = product/(substrate + product)

FIG.62A

Host (plasmid)	334(pRET22)	334(pRET22)	334(pRET22)	334(pRET22)
Added Substrate	50 μ M ALA	50 μ M PA	50 μ M EPA	50 μ M STA
	C18:3n-3	C18:0	C20:5n-3	C18:4n-3
Fatty Acid	% total lipid			
C16:0	13.91	15.06	16.92	20.08
C16:1	14.74	31.77	23.57	20.17
C18:0	4.06	*4.85	4.94	6.02
C18:1n-9	6.65	13.59	10.46	9.29
C18:3n-3	*38.66			*20.45
C18:4n-3				(12.57%)2.94
C20:4n-3				
C20:5n-3				
C22:5n-3			*15.48	
Total Lipid (μ g)	80	84	81	60

* indicates substrate added
 (% conversion) = product/(substrate + product)

FIG.62B

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Host(plasmid)	334(pRET-22+pCGR-4)	334(pYX242+pYES2)
Added Substrate	50 μ M GLA	50 μ M GLA
Fatty Acid	% total lipid	
C16:0	15.92	15.07
C16:1n-7	24.97	19.48
C18:0	8.25	6.48
C18:1n-7	3.9	1.61
C18:1n-9	18.48	12.71
C18:3n-6	*7.0	*10.54
C20:0	0	0
C20:3n-6	(27.81%) 4.36	(1.58%) 0.17
C20:4n-6	(27.55%) 4.32	0
Total Lipid(μ g)	508	168

*indicates substrate added
 (% conversion) = product/(substrate + product)

FIG.63A

Host(plasmid)	334(pRET-22+pCGR-4)	334(pYX242+pYES2)
Added Substrate	50 μ M STA	50 μ M STA
Fatty Acid	% total lipid	
C16:0	18.74	16.21
C16:1n-7	21.35	26.09
C18:0	6.78	7.57
C18:1n-7	1.97	1.7
C18:1n-9	20.73	22.41
C18:4n-3	*6.05	*13.43
C20:0	0	0.45
C20:4n-3	(15.88%) 1.68	(4.73 %) 0.69
C20:5n-3	(26.93%) 2.85	(3.22 %) 0.47
Total Lipid(μ g)	335	161

*indicates substrate added
 (% conversion) = product/(substrate + product)

FIG.63B